



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 103654**

**TO: Karen A Lacourciere**  
**Location: CM1/11D09&11E12**  
**Art Unit: 1635**  
**Saturday, September 13, 2003**

**Case Serial Number: 09/763590**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**CM1-6A06**  
**Phone: 605-1155**

**maryjane.ruhl@uspto.gov**

### **Search Notes**

Examiner Lacourciere,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
CM-1, Rm. 6-A-06  
605-1155

Search completed: September 13, 2003, 11:44:42  
Job time : 1985.73 secs

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

## FEATURES

Source

1. .206  
/organism="Tetraodon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone="219P01"  
/clone\_lib="G"  
/note="Genoscope sequence ID : C0AG219CH01SP1-end :  
PUC-ori"

BASE COUNT 58 a 42 c 48 g 46 t 12 others

## ORIGIN

Query Match 45.1%; Score 63.6; DB 29; Length 206;  
Best Local Similarity 74.2%; Pred. No. 3.4e-10;  
Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY 8 GUUCCGAGUGAGUGGUAUACGAGCGGCUAACACGCGAAAGGUCGCCGUGUCGAAA 67

Db 172 GTDTCGAGTAGTGTTATACGTTTCGCTACACGCGAAGGTCCCGGTTCGAAA 113

QY 68 CGGGC 73

Db 112 CGGGC 107

## RESULT 13

C13E10/c

## LOCUS

DEFINITION C13E10 590 bp DNA linear GSS 03-DEC-2000  
Ciona intestinalis genomic fragment, clone 3E10, genomic survey  
sequence.

## ACCESSION

AJ227180

## KEYWORDS

GSS; genome survey sequence.

## SOURCE

Ciona intestinalis

## ORGANISM

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.

## REFERENCE

1

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

3

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

4

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

5

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

6

AUTHORS

TITLE

JOURNAL

## source

1. .590  
/organism="Ciona intestinalis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7719"  
/clone="3E10"  
/dev\_stage="adult"

BASE COUNT 197 a 109 c 120 g 164 t

## ORIGIN

Query Match 45.0%; Score 63.4; DB 29; Length 590;  
Best Local Similarity 68.5%; Pred. No. 4.7e-10;  
Matches 50; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUAUACGAGCGGCUAACACGCGAAAGGUCGCCG 60

Db 441 ATCATCAGTTCCGTAAGTGTATCGTTTCGCTACACGCGAAGGTCCCGG 382

QY 61 UCGAAACCGGC 73

Db 381 TTCGAGCCCGGC 369

## RESULT 14

C11G6/c

## LOCUS

DEFINITION C11G6 617 bp DNA linear GSS 03-DEC-2000  
Ciona intestinalis genomic fragment, clone 11G6, genomic survey  
sequence.

## ACCESSION

AJ226216

## KEYWORDS

GSS; genome survey sequence.

## SOURCE

Ciona intestinalis

## ORGANISM

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.

## REFERENCE

1

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

3

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

4

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

5

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

6

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

7

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

vector: pBluescript KS.

Location/Qualifiers

1. .617

/organism="Ciona intestinalis"

/mol\_type="genomic DNA"

/db\_xref="taxon:7719"

/clone="11G6"

/dev\_stage="adult"

BASE COUNT 200 a 113 c 126 g 176 t 2 others

## ORIGIN





9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: [http://www.tigr.org/tldb/bac.ends/mouse/bac.end\\_intro.html](http://www.tigr.org/tldb/bac.ends/mouse/bac.end_intro.html)  
Plate: 144 row: M column: 11  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

source

Location/Qualifiers

1. .574

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="RPCI-23-144M11"

/sex="Female"

/lab\_host="DH10B"

/clone\_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site\_1:

ECORI; Site\_2: ECORI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of ECORI and ECORI Methyase. Size

selected DNA was cloned into the pBACe3.6 vector at the

ECORI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

143 a 136 c 129 g 166 t

BASE COUNT

ORIGIN

Query Match 45.7%; Score 64.4; DB 28; Length 574;

Best Local Similarity 74.2%; Pred. No. 2.2e-10;

Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY 8 GUUUCGUGAGUGUGUACACGUCGUAACACGCGAAGUCCCGGUCGAA 67

Db 382 GTTCCGTAGTGTAGTGTATACATTCGCTACACGCGAAGGTCGCCGTTGCGAA 323

QY 68 CCGGGC 73

Db 322 CCGGGC 317

RESULT 9

AZ989726

LOCUS

DEFINITION

2M0273K10F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0273K10 F, genomic survey sequence.

ACCESSION

AZ989726

VERSION

AZ989726.1 GI:13860953

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 695)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

UNPUBLISHED

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

TITLE

JOURNAL

COMMENT

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0273 row: K column: 10

Seq primer: CGTGTAAACGACGGCCACT

Class: plasmid ends

High quality sequence stop: 695.

Location/Qualifiers

1. .695

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0273K10"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gil4732114[gb]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

163 a 187 c 167 g 178 t

BASE COUNT

ORIGIN

Query Match 45.7%; Score 64.4; DB 28; Length 695;

Best Local Similarity 74.2%; Pred. No. 2.3e-10;

Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY 8 GUUUCGUGAGUGUGUACACGUCGUAACACGCGAAGUCCCGGUCGAA 67

Db 362 GTTCCGTAGTGTAGTGTATACATTCGCTACACGCGAAGGTCGCCGTTGCGAA 421

QY 68 CCGGGC 73

Db 422 CCGGGC 427

RESULT 10

CNS04TSI

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence T7 end of clone

038H13 of library A from Tetraodon nigroviridis, genomic survey

sequence.

ACCESSION

AL306891

VERSION

AL306891.1 GI:8208133

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;

Tetraodontidae; Tetraodontinae; Tetraodon.

1

Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Bernot,A., Fzames,C., Wincker,P., Brottier,P., Quetier,F.,

Saurin,W. and Weissenbach,J.

Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

REFERENCE

AUTHORS

TITLE

JOURNAL

**AUTHORS** Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Womack,J.E., de Jong,P.J. and Lewin,H.A.  
**TITLE** A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence  
**JOURNAL** Unpublished  
**COMMENT** Other\_GSSs: CH240\_70013.TV  
 Contact: Harris Lewin  
 Department of Animal Sciences  
 University of Illinois at Urbana Champaign  
 1201 W. Gregory Dr., Urbana, IL 61801, USA  
 Tel: 217 333 5998  
 Fax: 217 244 5617  
 Email: h-lewin@uiuc.edu  
 Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering.information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by the University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative).  
 Plate: 70 row: 0 column: 13  
 Seq primer: SP6  
 Class: BAC ends.  
**FEATURES** Location/Qualifiers  
 source  
 1. .201  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_70013"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site\_1: MboI; Site\_2: MboI; Hereford bull LI Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"  
 55 a 60 c .49 g 34 t 3 others  
**BASE COUNT** 55 a 60 c .49 g 34 t 3 others  
**ORIGIN**  
 Query Match 45.7%; Score 64.4; DB 29; Length 201;  
 Best Local Similarity 74.2%; Pred. No. 1.8e-10;  
 Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 GUUUCGUGAGUGGUAUCACGUCGCUUACACGCGAAAGGUCGCCGUGUCGAAA 67  
 Db 109 GTTTCGTAGTGTAGTGGTTATCAGCTTCGCTCACACGCGAAAGGTCGCCGTTTCGAAA 50  
 QY 68 CCGGGC 73  
 Db 49 CCGGGC 44  
**RESULT 7**  
 AZ115558/c  
 LOCUS AZ115558 232 bp DNA linear GSS 12-MAY-2000  
 DEFINITION RPCI-23-16D17.TV RPCI-23 Mus musculus genomic clone RPCI-23-16D17, genomic survey sequence.  
 ACCESSION AZ115558  
 VERSION AZ115558.1 GI:7776690  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 232)  
**REFERENCE** Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret  
**AUTHORS** B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.  
 Mouse BAC End Sequences from Library RPCI-23

**JOURNAL** Unpublished  
**COMMENT** Other\_GSSs: RPCI-23-16D17.TJ  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@tigr.org) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html  
 Plate: 16 row: D column: 17  
 Seq primer: T7  
 Class: BAC ends.  
**FEATURES** Location/Qualifiers  
 source  
 1. .232  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-16D17"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPCI-23"  
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."  
 55 a 57 c 54 g 66 t  
**BASE COUNT** 55 a 57 c 54 g 66 t  
**ORIGIN**  
 Query Match 45.7%; Score 64.4; DB 28; Length 232;  
 Best Local Similarity 74.2%; Pred. No. 1.9e-10;  
 Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 GUUUCGUGAGUGGUAUCACGUCGCUUACACGCGAAAGGUCGCCGUGUCGAAA 67  
 Db 180 GTTTCGTAGTGTAGTGGTTATCAGCTTCGCTAACACGCGAAAGGTCGCCGTTTCGAAA 121  
 QY 68 CCGGGC 73  
 Db 120 CCGGGC 115  
**RESULT 8**  
 AZ288311/c  
 LOCUS AZ288311 574 bp DNA linear GSS 27-JUL-2000  
 DEFINITION RPCI-23-144M11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-144M11, genomic survey sequence.  
 ACCESSION AZ288311  
 VERSION AZ288311.1 GI:9530097  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 574)  
**REFERENCE** Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret  
**AUTHORS** B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.  
 Mouse BAC End Sequences from Library RPCI-23  
**TITLE** Unpublished  
**JOURNAL** Other\_GSSs: RPCI-23-144M11.TV  
**COMMENT** Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research

```

Db      522  GTAGTTTCGGTAGTGTGTTATACGTTTCGCTACACGCGAAGGTCCTCCGGTTC 463
      64  GAAACCGGCGACUACAA 81
      462  GAAACCGGCGGAACAA 445

RESULT 4
LOCUS      BH305888/c
DEFINITION CH230-179P7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
VERSION    BH305888
KEYWORDS   BH305888.1 GI:17218296
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
REFERENCE  1 (bases 1 to 720)
AUTHORS    Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shwartsbeyn,
            A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
            Jong, P. and Fraser, C.M.
            Rat BAC End Sequences from Library CHORI-230 EcoRI segment
            Unpublished
            Other GSSs: CH230-179P7.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering.information.htm). BAC end
            plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 179 row: P column: 7
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
                1..720
                /organism="Rattus norvegicus"
                /mol_type="genomic DNA"
                /strain="BN/SsNhsd/MCW"
                /db_xref="taxon:10116"
                /clone="CH230-179P7"
                /sex="Female"
                /cell_type="Brain"
                /clone_lib="CHORI-230 Segment 1"
                /notes="Vector: PTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                CHORI-230 Rat (BN/SsNhsd/MCW) BAC library produced by
                Pieter de Jong"

BASE COUNT 188 a 179 c 151 g 202 t
ORIGIN

Query Match      47.0%; Score 66.2; DB 28; Length 720;
Best Local Similarity 71.8%; Pred. No. 5.9e-11;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY      3  CGUUGGUUCCGUGAGUGGUUAUCGUCGCUACACGCGAAGGTCCTCCGGTTC 62
      276  CATGAGTTTCGGTAGTGTGTTATACGTTTCGCTACACGCGAAGGTCCTCCGGTTC 217
      63  CGAACCAGGCG 73
      216  CGAACCAGGCG 206

Db      522  GTAGTTTCGGTAGTGTGTTATACGTTTCGCTACACGCGAAGGTCCTCCGGTTC 463
      64  GAAACCGGCGACUACAA 81
      462  GAAACCGGCGGAACAA 445

RESULT 5
LOCUS      AQ030852
DEFINITION HS_2182_B2_H05_MF CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2182 Col=10 Row=P, genomic survey
            sequence.
            AQ030852
            AQ030852.1 GI:3275778
            GSS.
            Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 390)
            Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
            Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
            Hood, L.
            Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
            Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
            99380589
            10449764
            Contact: Mahairas G.G., Wallace J.C., Hood L
            High throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2182 row: P column: 10
            Class: BAC ends
            High quality sequence stop: 390.
            Location/Qualifiers
                1..390
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Plate=2182 Col=10 Row=P"
                /sex="male"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in
                E-Coli DH10B"

BASE COUNT 104 a 82 c 83 g 120 t 1 others
ORIGIN

Query Match      46.4%; Score 65.4; DB 28; Length 390;
Best Local Similarity 74.6%; Pred. No. 9.7e-11;
Matches 50; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY      8  GUUUCUGUAGUGGUUAUCGUCGCUACACGCGAAGGTCCTCCGGTTC 67
      163  GTTCCGTTAGTGTGTTATACGTTTCGCTACACGCGAAGGTCCTCCGGTTC 222
      68  CCGGSCA 74
      223  CCGGSCA 229

Db      B2920607
      CH240_70013.TJ CHORI-240 Bos taurus genomic clone CH240_70013,
      genomic survey sequence.
      B2920607
      B2920607.1 GI:31645993
      GSS.
      Bos taurus (cow)
      Bos taurus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
      Bovidae; Bovinae; Bos.
      1 (bases 1 to 201)

```

```

FEATURES             Location/Qualifiers
  source              1..464
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4080340"
                    /tissue_type="glioblastoma"
                    /lab_host="DHI10B (T1 phage resistant)"
                    /clone_lib="NIH_MGC_57"
                    /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
                    SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc);
                    Double-stranded cDNA was prepared from cell line RNA.
                    5' and 3' adaptors were used in cloning as follows: 5'
                    adaptor sequence: 5'-ATCTAGAGCGGAGCGCCGACATG-dT(30)BN-3'
                    (where B = A, C, G, or T). Average
                    insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
                    contained inserts by PCR. This library was enriched for
                    full-length clones and was constructed by Clontech
                    Laboratories (Palo Alto, CA)."
```

BASE COUNT 138 a 110 c 160 g 55 t 1 others

ORIGIN

```

Query Match      52.98; Score 74.6; DB 10; Length 464;
Best Local Similarity 62.38; Pred. No. 1e-13;
Matches 76; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 2 CCGUUGGUUCCGUGAGUGUGUAUCACGUCGCUAACACGCGAAGGCGCCCGG 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 CCGGGGCTTCGTTAGTGTATACGTTTCGCTTACACGCGAAGGCTCCCGGT 86

QY 62 UCGAAGCGGCGACUACACACACACACACACUAGUAGGACCGAAGGCGGAACG 121
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 TCGAAGCGGCGGCGGACACACACACACACACACACACACACACACACACAACT 146

QY 122 GG 123
    ||
Db 147 GG 148

RESULT 2
AZ062238
LOCUS             582 bp DNA linear GSS 30-MAR-2000
DEFINITION       RPCI-23-404J7-TV RPCI-23 Mus musculus genomic clone RPCI-23-404J7,
genomic survey sequence.
ACCESSION        AZ062238
VERSION          AZ062238.1 GI:7353487
KEYWORDS         GSS.
SOURCE           Mus musculus (house mouse)
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE        1 (bases 1 to 582)
AUTHORS          Zhao,S., Nieman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
TITLE            Mouse BAC End Sequences from Library RPCI-23
JOURNAL           Unpublished
COMMENT          Other GSSs: RPCI-23-404J7.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACRAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/mouse/bac_end_intro.html
Plate: 404 row: J column: 7
```

```

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
  source              1..582
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="RPCI-23-404J7"
                    /sex="Female"
                    /lab_host="DHI10B"
                    /clone_lib="RPCI-23"
                    /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
                    EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                    brain genomic DNA was isolated and partially digested
                    with a combination of EcoRI and EcoRI Methylase. Size
                    selected DNA was cloned into the pBACE3.6 vector at the
                    EcoRI sites. The ligation products were transformed into
                    DHI10B electrocompetent cells (BRL Life Technologies)."
```

BASE COUNT 154 a 125 c 163 g 140 t

ORIGIN

```

Query Match      48.78; Score 68.6; DB 28; Length 582;
Best Local Similarity 68.78; Pred. No. 9.4e-12;
Matches 57; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

QY 2 CCGUUGGUUCCGUGAGUGUGUAUCACGUCGCUAACACGCGAAGGCGCCCGG 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 CCAGTGTTCGTTAGTGTATACGTTTCGCTTACACGCGAAGGCTCCCGGT 112

QY 62 UCGAAGCGGCGGCGACUACACACCA 84
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 TCGAAGCGGCGGCGGAAACAAGCA 135

RESULT 3
BX132357/c
LOCUS             767 bp DNA linear GSS 28-JAN-2003
DEFINITION       Danio rerio genomic clone DKEY-90F23, genomic survey sequence.
ACCESSION        BX132357
VERSION          BX132357.1 GI:27963631
KEYWORDS         GSS.
SOURCE           Danio rerio (zebrafish)
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE        1 (bases 1 to 767)
AUTHORS          Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE            Direct Submission
JOURNAL           Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humqu@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 90F23. 90F23 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
```

BASE COUNT 244 a 144 c 121 g 258 t

ORIGIN

```

Query Match      47.48; Score 66.8; DB 29; Length 767;
Best Local Similarity 69.28; Pred. No. 3.8e-11;
Matches 54; Conservative 17; Mismatches 7; Indels 0; Gaps 0;

QY 4 GUUGGUUCCGUGAGUGUGUAUCACGUCGCUAACACGCGAAGGCGCCCGG 63
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 09:43:56 ; Search time 1984.73 Seconds  
(without alignments)  
1726.650 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accguguuuccguagugu.....ggcacgugaaacgguuuu 141

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estlin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.6	52.9	464	10	BF244354
2	68.6	48.7	582	28	AZ062238
3	66.8	47.4	767	29	BX132357
4	66.2	47.0	720	28	BH305888

5	65.4	46.4	390	28	AQ030852
6	64.4	45.7	201	29	BZ920607
7	64.4	45.7	232	28	AZ115558
8	64.4	45.7	574	28	AZ288311
9	64.4	45.7	695	28	AZ989726
10	64.4	45.7	1101	29	CNS04751
11	64.2	45.5	595	13	BX297643
12	63.6	45.1	206	29	CNS0144U
13	63.4	45.0	590	29	C13E10
14	63.4	45.0	617	29	C111G6
15	62.6	44.4	543	13	BU712126
16	61.8	43.8	649	29	BX206800
17	61.6	43.7	418	28	AQ662870
18	61.6	43.7	761	13	BU711524
19	61.6	43.7	802	29	CNS030W4
20	61.6	43.7	897	29	CNS01XDW
21	61.6	43.7	1046	29	CNS04VSZ
22	61.6	43.7	1099	29	CNS05WY
23	61.6	43.7	1101	29	CNS05G97
24	61.2	43.4	467	9	AA489977
25	61.2	43.4	834	13	BW174938
26	60.2	42.7	780	13	BW170857
27	60.2	42.7	789	13	BW302287
28	60	42.6	771	29	BX176182
29	60	42.6	843	29	CNS05T4P
30	59.6	42.3	1101	29	CNS05AAR
31	59	41.8	1003	29	CNS051RL
32	58.8	41.7	568	29	CNS038GO
33	58.8	41.7	692	29	CNS023IT
34	58.6	41.6	981	29	CNS04CNF
35	58.6	41.6	987	29	CNS0500S
36	58.6	41.6	1002	29	CNS056ED
37	58.4	41.4	610	29	DR16F6S
38	58.2	41.3	918	29	CNS0281P
39	58.2	41.3	946	29	CNS023IS
40	58	41.1	338	13	BW166952
41	58	41.1	363	13	BW296387
42	58	41.1	763	28	BH063051
43	57.2	40.6	935	29	CNS045M0
44	56.8	40.3	819	29	BX232148
45	55.8	39.6	936	29	CC142986

# ALIGNMENTS

RESULT 1  
BF244354  
LOCUS  
DEFINITION  
601862918F1 NIH\_MGC\_57 Homo sapiens CDNA clone IMAGE:4080340 5', linear EST 14-NOV-2000  
mRNA sequence.  
ACCESSION  
BF244354  
VERSION  
BF244354.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 464)  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE  
Unpublished  
JOURNAL  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
COMMENT  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L10M940 row: d column: 05  
High quality sequence stop: 142.

BF244354 464 bp mRNA linear EST 14-NOV-2000  
601862918F1 NIH\_MGC\_57 Homo sapiens CDNA clone IMAGE:4080340 5',  
mRNA sequence.  
BF244354  
BF244354.1 GI:11158272  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L10M940 row: d column: 05  
High quality sequence stop: 142.

; LENGTH: 4887 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1278..4013  
US-08-005-002C-7

Query Match 21.7%; Score 30.6; DB 1; Length 4887;  
Best Local Similarity 46.4%; Pred. No. 0.19;  
Matches 32; Conservative 13; Mismatches 24; Indels 0; Gaps 0;  
QY 5 UUGGUUCCGUGAGUGUGUUAUCACGUCGCCUAACACGCGAAGGUCCCGGUUCG 64  
Db 4247 TTGGTTTCGGTGGTCTAGTCGGTTATGCGATCTGCTTAACACGCGAAGCTCCCGATTGG 4188  
QY 65 AAACCGGGC 73  
Db 4187 ATCTGGGC 4179

Search completed: September 13, 2003, 08:06:12  
Job time : 64.5109 secs







## RESULT 11

```

US-09-107-532A-488/c
/ Sequence 488, Application US/09107/532A
/ Patent No. 6583275
/ GENERAL INFORMATION:
/ APPLICANT: Lynn A Doucette-Stamm and David Bush
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
/ ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
/ NUMBER OF SEQUENCES: 7310
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: GENOME THERAPEUTICS CORPORATION
/ STREET: 100 Beaver Street
/ CITY: Waltham
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02354
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: CD-ROM ISO9660
/ COMPUTER: PC
/ OPERATING SYSTEM: <Unknown>
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/107,532A
/ FILING DATE: 30-Jun-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/085,598
/ FILING DATE: 14 May 1998
/ APPLICATION NUMBER: 60/051571
/ FILING DATE: July 2, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ariniello, Pamela Deneka
/ REGISTRATION NUMBER: 40,489
/ REFERENCE/DOCKET NUMBER: GTC-012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (781)893-5007
/ TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 488:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 186 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Enterococcus faecium
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (b) LOCATION 1...186
/ SEQUENCE DESCRIPTION: SEQ ID NO: 488:
/
US-09-107-532A-488

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-512-861A-8

Query Match      29.2%; Score 41.2; DB 3; Length 146;
Best Local Similarity 70.0%; Pred. No. 7.5e-06;
Matches 70; Conservative 0; Mismatches 28; Indels 2; Gaps 1;

QY 28 AUCAGGUCGCCUUAACACGCGAAGGUCGCCGUAACACCGGGGACUACAAACCAACA 87
Db 28 AGCGUGUGGCCCAUAACACGAGGUCGGAUGGAUCCAAACCCGGA--UCGUCACGGCG 85

QY 88 CACAACACUGAUGAGGACCGCAAGGUCGGAAGGCGGACG 127
Db 86 CACAACACUGAUGAGGACCGCAAGGUCGGAAGGCGGACG 125

RESULT 9
US-08-512-861A-14
; Sequence 14, Application US/08512861A
; Patent No. 6146885
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-512-861A-14

Query Match      29.2%; Score 41.2; DB 3; Length 167;
Best Local Similarity 67.4%; Pred. No. 7.8e-06;
Matches 58; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 49 AAAGUCCCGGUGUACGCGGCAACACGCGGCAACACACACACACACACACACACAC 108
Db 66 AACCAUCUCUGUGUGUACGCGGCAACACGCGGCAACACACACACACACACACACAC 125

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-270-076A-2

Query Match      24.4%; Score 34.4; DB 1; Length 1483;
Best Local Similarity 55.9%; Pred. No. 0.005;
Matches 38; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 14 GUAGUGUAGUGUUAUCACGUCGUACGCGGAAAGGUCGCCGUAACACCGGGC 73
Db 41 GTGCGGTACTCGTAGCGGCTCCCTTAGCATGGAGAGGTCTCCGTTCCGATTCGCGAC 100

QY 74 ACUACAAA 81
Db 101 TCGTCAA 108

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-270-076A-2

Query Match      24.4%; Score 34.4; DB 1; Length 1483;
Best Local Similarity 55.9%; Pred. No. 0.005;
Matches 38; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 14 GUAGUGUAGUGUUAUCACGUCGUACGCGGAAAGGUCGCCGUAACACCGGGC 73
Db 41 GTGCGGTACTCGTAGCGGCTCCCTTAGCATGGAGAGGTCTCCGTTCCGATTCGCGAC 100

QY 74 ACUACAAA 81
Db 101 TCGTCAA 108

```

```

;
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-10

```

```

Query Match 30.2%; Score 42.6; DB 3; Length 171;
Best Local Similarity 67.6%; Pred. No. 2.4e-06;
Matches 75; Conservative 0; Mismatches 34; Indels 2; Gaps 1;

```

```

QY 28 AUCACGUUGCCUUAACACACGGAAGGUCGCCGUAACCGGGGCGACUACAAACCAACA 87
Db 28 AGCGUGCGGCCCAUAACCCAGAGGUCGAGGUAUGGAAACCCCGGA--UCGUACCGCGG 85
QY 88 CACAACACUGAUGAGGACGACGGAAGGUCGGAACGGGCGACGCGGAACCGU 138
Db 86 CACAACACUGAUGAGGACGACGGAAGGUCGGAACGGGCGAGGUAUACGAA 136

```

```

RESULT 7
US-08-512-861A-4
; Sequence 4, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994

```

```

; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-4

```

```

Query Match 29.2%; Score 41.2; DB 3; Length 146;
Best Local Similarity 70.0%; Pred. No. 7.5e-06;
Matches 70; Conservative 0; Mismatches 28; Indels 2; Gaps 1;

```

```

QY 28 AUCACGUUGCCUUAACACACGGAAGGUCGCCGUAACCGGGGCGACUACAAACCAACA 87
Db 28 AGCGUGCGGCCCAUAACCCAGAGGUCGAGGUAUGGAAACCCCGGA--UCGUACCGCGG 85
QY 88 CACAACACUGAUGAGGACGACGGAAGGUCGGAACGGGCGACG 127
Db 86 CACAACACUGAUGAGGACGACGGAAGGUCGGAACGGGCGAGG 125

```

```

RESULT 8
US-08-512-861A-8
; Sequence 8, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146

```

Query Match 49.5%; Score 69.8; DB 3; Length 132;  
Best Local Similarity 72.6%; Pred. No. 2.9e-16;  
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ACCGUGUUCGUGAGUGUUAUCACGUCGUAACACGCGGAAAGGUCGCCGG 60  
Db 11 ACCGTTGTTCCGTAGTGTAGTATCATCGCTCCACACGCGGACGCTCCCGG 70  
QY 61 UUCGAAACCGGCG 73  
Db 71 TTCGAAACCGGCG 83

RESULT 4  
PCT-US94-05700-17  
; Sequence 17, Application PC/TUS9405700  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; TITLE OF INVENTION: RIBOZYME GENE THERAPY FOR HIV INFECTION AND AIDS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBBINS, BERLINER & CARSON  
; STREET: 201 NORTH FIGUEROA STREET  
; CITY: LOS ANGELES  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/05700  
; FILING DATE: 17 MAY 1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BERLINER, ROBERT  
; REGISTRATION NUMBER: 20,121  
; REFERENCE/DOCKET NUMBER: 5555-209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 213-977-1001  
; TELEFAX: 213-977-1003  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 133 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 97  
; OTHER INFORMATION: /note= "W = INTERNAL NUCLEOTIDE  
; OTHER INFORMATION: SEQUENCE"  
PCT-US94-05700-17

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Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;  
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QY 61 UUCGAAACCGGCG 73  
Db 71 TTCGAAACCGGCG 83

RESULT 5  
US-08-512-861A-6  
; Sequence 6, Application US/08512861A

; Patent No. 6146886  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED  
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
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; APPLICATION NUMBER: US/08/512,861A  
; FILING DATE: August 8, 1995  
; PRIOR APPLICATION DATA: Two  
; APPLICATION NUMBER: 08/293,520  
; FILING DATE: August 19, 1994  
; APPLICATION NUMBER: 08/337,608  
; FILING DATE: No. 6146886ember 10, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 215/154  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 171  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-512-861A-6

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QY 88 CACAACACUGAUGAGGACGCGGAAAGGUCGAAACCGGCGCACGUGGAAACCGU 138  
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; Sequence 10, Application US/08512861A  
; Patent No. 6146886  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED  
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.

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; OTHER INFORMATION: /note= "insertion location of
; OTHER INFORMATION: foreign gene in pol III
; OTHER INFORMATION: transcription cassette in
; OTHER INFORMATION: vector pMT"
US-08-245-742A-17

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Best Local Similarity 72.6%; Pred. No. 2.9e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

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QY 61 UUCGAAACCGGGC 73
Db 71 TTCGAAACCGGGC 83

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US-08-465-483-17
; Sequence 17, Application US/08465483
; Patent No. 5811275
; GENERAL INFORMATION:
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Yu, Mang
; APPLICANT: Yamada, Osamu
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Leavitt, Mark
; APPLICANT: Ho, Anthony
; TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
; TITLE OF INVENTION: and AIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,483
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,465
; FILING DATE: 17-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,742
; FILING DATE: 17-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 2307E-567-11
; TELEPHONE: (415) 543-9600
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: (96^97)
; OTHER INFORMATION: /note= "insertion location of
; OTHER INFORMATION: foreign gene in pol III
; OTHER INFORMATION: transcription cassette in
; OTHER INFORMATION: vector pMT"
US-08-245-742A-17
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; OTHER INFORMATION: foreign gene in pol III
; OTHER INFORMATION: transcription cassette in
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US-08-465-483-17

Query Match          49.5%; Score 69.8; DB 1; Length 132;
Best Local Similarity 72.6%; Pred. No. 2.9e-16;
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

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Db 11 ACCGTTGGTTCCGTTAGTGTAGTGTATACGTTCCGCTCACACGCGAAGGTCGCCGG 70
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QY 61 UUCGAAACCGGGC 73
Db 71 TTCGAAACCGGGC 83

RESULT 3
US-08-876-996-17
; Sequence 17, Application US/08876996
; Patent No. 6132962
; GENERAL INFORMATION:
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Yu, Mang
; APPLICANT: Yamada, Osamu
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Leavitt, Mark
; APPLICANT: Ho, Anthony
; TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
; TITLE OF INVENTION: and AIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,996
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,742
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 2307E-567-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: (96^97)
; OTHER INFORMATION: /note= "insertion location of
; OTHER INFORMATION: foreign gene in pol III
; OTHER INFORMATION: transcription cassette in
; OTHER INFORMATION: vector pMT"
US-08-876-996-17
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 569978 seqs, 220691566 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	69.8	49.5	133	5	PCT-US94-05700-17
5	42.6	30.2	171	3	US-08-512-861A-6
6	42.6	30.2	171	3	US-08-512-861A-10
7	41.2	29.2	146	3	US-08-512-861A-4
8	41.2	29.2	146	3	US-08-512-861A-8
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12	32.6	23.1	1230025	4	US-09-198-452A-1
13	31.6	22.4	702	3	US-08-998-416-947
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25	28.6	20.3	1230025	4	US-09-198-452A-1
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27	28.4	20.1	38155	4	US-09-453-702B-79

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	33	27.6	19.6	16885	1	US-08-390-878-16	Sequence 16, Appli
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	36	27.4	19.4	21338	4	US-08-961-527-20	Sequence 20, Appli
	37	27.2	19.3	9472	4	US-08-150-204E-96	Sequence 96, Appli
	38	27	19.1	13865	3	US-09-009-217-11	Sequence 11, Appli
	39	27	19.1	13865	3	US-09-009-656-11	Sequence 11, Appli
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	43	26.6	18.9	724	5	PCT-US96-06583-98	Sequence 98, Appli
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## ALIGNMENTS

RESULT 1  
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; Sequence 17, Application US/08245742A  
; Patent No. 5670361  
; GENERAL INFORMATION:  
; APPLICANT: Wong-Staal, Flossie  
; APPLICANT: Yu, Mang  
; APPLICANT: Yamada, Osamu  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Leavitt, Mark  
; APPLICANT: Ho, Anthony  
; TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection  
; TITLE OF INVENTION: and AIDS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/245,742A  
; FILING DATE: 17-MAY-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/062,465  
; FILING DATE: 17-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 2307E-567-10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY:  
; LOCATION: (96^97)

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ACCESSION	BU712126
VERSION	BU712126.1 GI:28319513
KEYWORDS	EST.
SOURCE	Schistosoma japonicum
ORGANISM	Schistosoma japonicum
REFERENCE	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS	Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma. 1 (bases 1 to 543) Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J., Sun,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Ou,J., Xu,Z., Huang,J., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han, Z.
TITLE	Expressed sequence tags from adults of Schistosoma japonicum
JOURNAL	Unpublished
COMMENT	Contact: Zeqiang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhongjiang Hi-tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@hgsc.sh.cn.

S. japonicum sequences.			
BASE COUNT	183 a	109 c	90 q 160 t
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Best Local Similarity 69.6%; Pred. No. 3.6e-10;
Matches 48; Conservative 17; Mismatches 4; Indels 0; Gaps 0
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Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 Genome Res. 10 (7), 939-949 (2000)  
 20359837  
 10899143  
 3 (bases 1 to 1101)  
 Genoscope.  
 Direct Submission  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 ORGANISM  
 COMMENT  
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.  
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 Db 772 CCGGCG 777  
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 BX297643/c  
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 BX297643  
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 EST.  
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 REFERENCE  
 1 (bases 1 to 595)  
 Govoroun, M., Guiguen, Y. and Le Gac, F.  
 Construction and primary characterization of normalized cdna libraries in rainbow trout, *Oncorhynchus mykiss*  
 Unpublished  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 ORGANISM  
 COMMENT  
 Contact: Guiguen Y  
 INRA - SCRIBE  
 Campus de Beaulieu, RENNES cedex, 35042, France  
 Tel: 02.23.48.50.09  
 Fax: 02.23.48.50.20  
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
 Sequence cleaned of vector, adaptor and repetitions. Contact us at [sigenasupport@jouy.inra.fr](mailto:sigenasupport@jouy.inra.fr) to obtain the chromatogram of this sequence.  
 Plate: 0002 row: 1 column: 4  
 Seq primer: M13F.  
 Location/Qualifiers  
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 /note="Vector: p7T3D-pac; Clone distribution : AGENAE Resource centre, Francois PIUMI, Francois.Plumie@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (UREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"  
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 Query Match 47.6%; Score 64.2; DB 13; Length 595;  
 Best Local Similarity 71.0%; Pred. No. 1.1e-10;  
 Matches 49; Conservative 17; Mismatches 3; Indels 0; Gaps 0;  
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 RESULT 12  
 CNS0124U/c  
 LOCUS  
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 ALI73847  
 VERSION  
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 GSS; genome survey sequence.  
 SOURCE  
 Tetraodon nigroviridis  
 ORGANISM  
 Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.  
 REFERENCE  
 1  
 Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)  
 20296633  
 PUBMED  
 REFERENCE  
 2  
 10835645  
 Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 Genome Res. 10 (7), 939-949 (2000)  
 20359837  
 10899143  
 3 (bases 1 to 206)  
 Genoscope.  
 Direct Submission  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 ORGANISM  
 COMMENT  
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis

TITLE	Mouse BAC End Sequences from Library RPCI-23
JOURNAL	unpublished
COMMENT	Other_GSSs: RPCI-23-16D17.TJ Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 7912 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library library availability, please contact Pieter (pieter@jeong.med.buffalo.edu). Clones may BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu">http://bacpac.med.buffalo.edu</a> ). Clones may or from Resea ch Genetics ( <a href="http://inforesgen.com">inforesgen.com</a> ). <a href="http://www.tigr.org/tdb/bac_ends/mouse/bac_e">http://www.tigr.org/tdb/bac_ends/mouse/bac_e</a> plate: 16 row: D column: 17

```

Class: BAC ends.
Location/Qualifiers
1..232
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="RPC1-23-16D17"
  /sex="Female"
  /lab_host="DH10B"
  /clone_lib="RPC1-23"
  /note="Organ: Kidney/Brain; Vector: pBACE3.6; site_1:
  EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
  brain genomic DNA was isolated and partially digested
  with a combination of EcoRI and EcoRI Methylase. Size
  selected DNA was cloned into the pBACE3.6 vector at the
  EcoRI sites. The ligation products were transformed into
  DH10B electrocompetent cells (BRL Life Technologies)."
55 a 57 c 54 g 66 t

BASE COUNT
ORIGIN
Query Match 47.7%; Score 64.4; DB 28; Length 232;
Best Local Similarity 74.2%; Fred. No. 7.5e-11;
Matches 49; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY 8 GGUUCCGAGUGUAGUGUATUACACGUCGUCCUATACACCGGAAGGUCGCCGGUUCGAA 67
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 GTTCCGAGTGTAGTGGTATACATTCGCTTAACACCGGAAGGTCCCCGGTTCGAA 121
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 68 CCGGGC 73
    |||||
Db 120 CCGGGC 115
    |||||

```

The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPcI-23. For BAC library availability, please contact Pieter de Jong ([pieterdejong.med.buffalo.edu](mailto:pieterdejong.med.buffalo.edu)). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics ([inforesgen.com](http://inforesgen.com)). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)

Plate: 144 row: M column: 11

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers
1. 574
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/mol.type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPcI-23-144M11"
/sex="Female"
/lab_host="DH10B"
/clone.lib="RPcI-23"
/note="Organ: Kidney/Brain; Vector: pBACE3 6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

[illegible]

RESULT 10	ACCESSION	REFERENCE	TITLE
CNS04TSI	VERSION	AUTHORS	JOURNAL
LOCUS	KEYWORDS		MEDLINE
DEFINITION	SOURCE		PUBMED
	ORGANISM		REFERENCE
			AUTHORS

plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0273 row: K column: 10  
 Seq primer: CGTTGTAAACACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 695.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0273K10"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PW042nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (G1/4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 163 a 187 c 167 g 178 t  
 ORIGIN

Query Match 48.0%; Score 64.8; DB 28; Length 695;  
 Best Local Similarity 69.7%; Pred. No. 7 1e-11;  
 Matches 53; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 8 GUUUCGGUAGUGUAGUGUUACACGUUCGCCUACACGCGAAGUCCCGGUUCGAAA 67  
 Db 1:::|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||  
 362 GTTTCGTAGTAGTGTGTTATCAGCTTCGCTCACACGCGAAGGTCGCCGTTGCGAAA 421

QY 68 CGGGGCACUACAACA 83  
 Db ||||| | | ||  
 422 CGGGCGGGAACAGCA 437

RESULT 7  
 BZ920607/c  
 LOCUS  
 DEFINITION  
 genomic survey sequence.  
 ACCESSION  
 BZ920607  
 VERSION  
 BZ920607.1 GI:31645993  
 KEYWORDS  
 GSS.  
 SOURCE  
 Bos taurus (cow)  
 ORGANISM  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bovinae; Bos.

```

Db      462 GAAACCGGGCGGAAACAA 445
|||||
BH305888      720 bp      DNA      linear      GSS 30-NOV-2001
CH230-179P7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-179P7, genomic survey sequence.
ACCESSION      BH305888
VERSION        BH305888
KEYWORDS       BH305888.1 GI:17218296
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus
REFERENCE      1 (bases 1 to 720)
AUTHORS        Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
                A., Gebregorjais, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
                Jong, P., and Fraser, C.M.
                Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                Unpublished
                Other GSSs: CH230-179P7.TJ
                Contact: Shaying Zhao
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Dr., Rockville, MD 20850, USA
                Tel: 301 838 0200
                Fax: 301 838 0208
                Email: szhao@tigr.org
                Clones are derived from the rat BAC library CHORI-230
                (http://www.chori.org/bacpac/rat230.htm). For BAC library
                availability, please contact Pieter de Jong (pjejong@email.cbo.org).
                Clones may be purchased from BACPAC Resources
                (http://www.chori.org/bacpac/or_ering_information.htm). BAC end
                page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
                Plate: 179 row: P column: 7
                Seq primer: T7
                Class: BAC ends.
                Location/Qualifiers
                1..720
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                /sex="Female"
                /cell_type="Brain"
                /clone_lib="CHORI-230 Segment 1"
                /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
                Pieter de Jong"
BASE COUNT      188 a 179 c 151 g 202 t
ORIGIN
Query Match      49.0%; Score 66.2; DB 28; Length 720;
Best Local Similarity 71.8%; Pred. No. 2.4e-11;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY      3 CGUUGUUUCCGUGAGUGGUUAUACGUGCCUACACGCGAAGGUCGCCGUGU 62
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      276 CATGAGTTCCGTAGTGTGTTATCAGTTTCCTTAACACGCGAAGGTCGCCG 217
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      63 CGAAACCGGCG 73
        |||||
Db      216 CGAAACCGGCG 206
        |||||

RESULT 5
LOCUS      AQ030852
DEFINITION HS_2182_B2_H05_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2182 Col=10 Row=P, genomic survey
sequence.
ACCESSION      AQ030852
VERSION        AQ030852.1 GI:3275778
KEYWORDS       GSS.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 390)
AUTHORS        Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                Kellier, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
                Hood, L.
                Sequence-tagged connectors: A sequence approach to mapping and
                scanning the human genome
                Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                99380589
                MEDLINE
                PUBMED
                10449764
                COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
                High Throughput Sequencing Center
                University of Washington
                401 Queen Anne Avenue North, Seattle, WA 98109, USA
                Tel: (206) 616-3618
                Fax: (206) 616-3887
                Email: jwallace@u.washington.edu
                Sequence Tagged Connector
                Plate: 2182 Row: P column: 10
                Class: BAC ends
                High quality sequence stop: 390.
                Location/Qualifiers
                1..390
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Plate=2182 Col=10 Row=P"
                /sex="male"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                E-Coli DH10B"
BASE COUNT      104 a 82 c 83 g 120 t 1 others
ORIGIN
Query Match      48.4%; Score 65.4; DB 28; Length 390;
Best Local Similarity 74.6%; Pred. No. 3.9e-11;
Matches 50; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

QY      8 GUUUCGUGAGUGGUUAUACGUGCCUACACGCGAAGGUCGCCGUGUUGAAA 67
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      163 GTTCCGTAGTGTGTTATCAGTTTCCTTAACACGCGAAGGTCGCCGTT 222
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      68 CCGGGCA 74
        |||||
Db      223 CCGGGCA 229
        |||||

RESULT 6
LOCUS      AZ989726
DEFINITION 2M0273K10F Mouse 10kb plasmid UUC2M library Mus musculus genomic
clone UUGC2M0273K10 F, genomic survey sequence.
ACCESSION      AZ989726
VERSION        AZ989726.1 GI:13860953
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1 (bases 1 to 695)
AUTHORS        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
                M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
                and Wright, D., Weiss, R.
                Mouse whole genome scaffolding with paired end reads from 10kb

```

FEATURES source

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 09:43:56 ; Search time 1900.27 Seconds  
(without alignments)  
1726.650 Million cell updates/sec

Title: US-09-763-590-1

Perfect score: 135

Sequence: 1 accguuguuuccguagu.....ggcacgucggaacgguuu 135

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_eston:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_nam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	71	52.6	464	10	BF244354
2	67.2	49.8	582	28	AZ062238
c 3	66.8	49.5	767	29	BX132357
c 4	66.2	49.0	720	28	BH305888

5	65.4	48.4	390	28	AQ030852
6	64.8	48.0	695	28	AZ989726
c 7	64.4	47.7	201	29	BZ920607
c 8	64.4	47.7	232	28	AZ115558
c 9	64.4	47.7	574	28	AZ288311
c 10	64.4	47.7	1101	29	CNS04751
c 11	64.2	47.6	595	13	BX297643
c 12	63.6	47.1	206	29	CNS01240
c 13	63.4	47.0	590	29	C13E10
c 14	63.4	47.0	617	29	C11IG6
15	62.6	46.4	543	13	BU712126
16	61.8	45.8	649	29	BX206800
17	61.6	45.6	418	28	AO662870
c 18	61.6	45.6	761	13	BU711524
19	61.6	45.6	802	29	CNS030M4
20	61.6	45.6	897	29	CNS01XDM
21	61.6	45.6	1046	29	CNS04YSZ
22	61.6	45.6	1099	29	CNS05MVY
23	61.6	45.6	1101	29	CNS05G97
c 24	61.2	45.3	467	9	AA489977
c 25	61.2	45.3	834	13	BW174938
c 26	60.2	44.6	771	29	BX176182
c 27	60.2	44.6	780	13	BW170857
c 28	60.2	44.6	789	13	BW302287
29	60	44.4	843	29	CNS0574P
30	59.6	44.1	1101	29	CNS05AAR
31	59	43.7	1003	29	CNS051R1
c 32	58.8	43.6	568	29	CNS038G0
c 33	58.8	43.6	692	29	CNS023IT
c 34	58.6	43.4	981	29	CNS04CNF
c 35	58.6	43.4	987	29	CNS0500S
36	58.6	43.4	1002	29	CNS056ED
c 37	58.4	43.3	610	29	DR16F6S
c 38	58.2	43.1	918	29	CNS0281P
c 39	58.2	43.1	946	29	CNS0231S
40	58	43.0	338	13	BW166952
c 41	58	43.0	333	13	BW296387
c 42	58	43.0	763	28	BH063051
c 43	57.2	42.4	935	29	CNS045M0
c 44	56.2	41.6	791	29	CC127410
c 45	55.8	41.3	819	29	BX232148

## ALIGNMENTS

RESULT 1  
BF244354  
LOCUS  
DEFINITION 601862918F1 NIH\_MGC\_57 Homo sapiens cDNA clone IMAGE:4080340 5',  
464 bp mRNA linear EST 14-NOV-2000  
BF244354  
mRNA sequence.  
ACCESSION  
VERSION BF244354.1 GI:11158272  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1. (bases 1 to 464)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [graphs-r@mail.nih.gov](mailto:graphs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LICM940 row: d column: 05  
High quality sequence stop: 142.

Qy 68 CCGGGCACUACAAACA 83  
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Db 170 CCGGTCGGGACCGCCA 185

Search completed: September 13, 2003, 09:43:36  
Job time : 166.25 secs





Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
US-10-027-632-135532	45.38%	61.2	DB 13	818	0	0	0
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
Matches	46	Conservative	17	Mismatches	3	Indels	0
QY	6	UGGUUCCGAGUGAGUGGUUACACGUCGUCURACACGCGAAAGGUCGCCGGUUCGA	65				
DB	239	TGGTTTCGTAGTGTAGTGTATCATGTTGGCTCACGCGAAAGGTCGCCGGTTCGA	298				
QY	66	AACCGG 71					
DB	299	RACTGG 304					
RESULT 9	US-10-027-632-135532/c						
Sequence	135532, Application	US/10027632					
GENERAL INFORMATION:							
APPLICANT:	Wang, David G.						
TITLE OF INVENTION:	Identification and Mapping of Single Nucleotide						
FILE REFERENCE:	108827.129						
CURRENT APPLICATION NUMBER:	US/10/027.632						
CURRENT FILING DATE:	2002-04-30						
PRIOR APPLICATION NUMBER:	US 60/218,006						
PRIOR FILING DATE:	2000-07-12						
PRIOR APPLICATION NUMBER:	US 60/198,676						
PRIOR FILING DATE:	2000-04-20						
PRIOR APPLICATION NUMBER:	US 60/193,483						
PRIOR FILING DATE:	1999-11-23						
PRIOR APPLICATION NUMBER:	US 60/156,358						
PRIOR FILING DATE:	1999-09-28						
PRIOR APPLICATION NUMBER:	US 60/146,002						
PRIOR FILING DATE:	1999-08-09						
NUMBER OF SEQ ID NOS:	325720						
SOFTWARE:	FastSeq for Windows Version 4.0						
SEQ ID NO	135532						
LENGTH:	603						
TYPE:	DNA						
ORGANISM:	Human						
US-10-027-632-135532	37.5%	50.6	DB 13	Length 603	0	0	0
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
Matches	40	Conservative	16	Mismatches	9	Indels	0
QY	8	GUUUCGAGUGAGUGGUUACACGUCGUCURACACGCGAAAGGUCGCCGGUUCGAA	67				
DB	136	GTTTCGTAGTGTAGTGTATCATGTTGGCTCACGCGAAAGGTCGCCGGTTCGA	77				
QY	68	CCGG 72					
DB	76	CCAGG 72					
RESULT 10	US-10-027-632-135520						
Sequence	135520, Application	US/10027632					
GENERAL INFORMATION:							
APPLICANT:	Wang, David G.						
TITLE OF INVENTION:	Identification and Mapping of Single Nucleotide						
FILE REFERENCE:	108827.129						
CURRENT APPLICATION NUMBER:	US/10/027.632						
CURRENT FILING DATE:	2002-04-30						
PRIOR APPLICATION NUMBER:	US 60/218,006						
PRIOR FILING DATE:	2000-07-12						
PRIOR APPLICATION NUMBER:	US 60/198,676						

; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13960  
 ; LENGTH: 704  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-13960

Query Match 48.7%; Score 65.8; DB 13; Length 704;  
 Best Local Similarity 71.8%; Pred. No. 1.1e-13;  
 Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 CGUUGGUUCCGAGUGUAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUU 62  
 Db 301 YCAGGTTTCCTAGTGTAGTGTATCATCGTTCGCTCACACGCGAAAGGTCGCCGTT 242  
 QY 63 CGAAACCGGGC 73  
 Db 241 CGAAACCGGGC 231

## RESULT 6

US-10-027-632-13961/G  
 ; Sequence 13961, Application US/10027632  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; PRIOR FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13961  
 ; LENGTH: 704  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-13961

Query Match 48.7%; Score 65.8; DB 13; Length 704;  
 Best Local Similarity 71.8%; Pred. No. 1.1e-13;  
 Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 CGUUGGUUCCGAGUGUAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUU 62  
 Db 301 YCAGGTTTCCTAGTGTAGTGTATCATCGTTCGCTCACACGCGAAAGGTCGCCGTT 242  
 QY 63 CGAAACCGGGC 73  
 Db 241 CGAAACCGGGC 231

## RESULT 7

US-10-027-632-150959

; Sequence 150959, Application US/10027632  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; PRIOR FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 150959  
 ; LENGTH: 818  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-150959

Query Match 45.3%; Score 61.2; DB 13; Length 818;  
 Best Local Similarity 69.7%; Pred. No. 5e-12;  
 Matches 46; Conservative 17; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 UGGUUCGAGUGUAGUGUUAUCACGUCGCUAACACGCGAAAGGUCGCCGGUU 65  
 Db 239 TGGTTCCGAGTGTAGTGTATCATCGTTCGCTCACACGCGAAAGGTCGCCGTT 298  
 QY 66 AACCGG 71  
 Db 299 AACTGG 304

## RESULT 8

US-10-027-632-150960  
 ; Sequence 150960, Application US/10027632  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; PRIOR FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 150960  
 ; LENGTH: 818  
 ; TYPE: DNA  
 ; ORGANISM: Human

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US-09-974-974-17
; Sequence 17, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; FILE REFERENCE: target RNA by recognizing another molecule
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 138
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal T-mL
US-09-974-974-17

Query Match
Best Local Similarity 61.3%; Score 82.8; DB 11; Length 138;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUCCGAGUGAGUGUUAUCACGUGCCUAAACACGCGAAAGGUGCCCGG 60
Db 1 ACCGUGGUGUCCGAGUGAGUGUUAUCACGUGCCUAAACACGCGAAAGGUGCCCGG 60
QY 61 UUCGAAACCGGCGACUACACAA 86
Db 61 UUCGAAACCGGCGACUACAAACCA 86

RESULT 3
US-10-027-632-13958/c
; Sequence 13958, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13958
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13958

Query Match
Best Local Similarity 48.7%; Score 65.8; DB 13; Length 704;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGUUGGUGUCCGAGUGAGUGUUAUCACGUGCCUAAACACGCGAAAGGUGCCCGG 62
Db 301 YCAGGTTTCCTAGTGTAGTGTATCAGTTCGCTCACACACGCGAAAGGTTCCCGGTT 242
QY 63 CGAAACCGGGC 73
Db 241 CGAAACCGGGC 231

RESULT 4
US-10-027-632-13959/c
; Sequence 13959, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13959
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13959

Query Match
Best Local Similarity 71.8%; Score 65.8; DB 13; Length 704;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGUUGGUGUCCGAGUGAGUGUUAUCACGUGCCUAAACACGCGAAAGGUGCCCGG 62
Db 301 YCAGGTTTCCTAGTGTAGTGTATCAGTTCGCTCACACACGCGAAAGGTTCCCGGTT 242
QY 63 CGAAACCGGGC 73
Db 241 CGAAACCGGGC 231

RESULT 5
US-10-027-632-13960/c
; Sequence 13960, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13958
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13958

Query Match
Best Local Similarity 48.7%; Score 65.8; DB 13; Length 704;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

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Title: US-09-763-590-1

Perfect score: 135

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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12: /cgn2\_6/ptodata/2/pubpna/US09D\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.8	61.3	88	11	US-09-974-974-5
2	82.8	61.3	138	11	US-09-974-974-17
3	85.8	48.7	704	13	US-10-027-632-13958
4	65.8	48.7	704	13	US-10-027-632-13959
5	65.8	48.7	704	13	US-10-027-632-13960
6	65.8	48.7	704	13	US-10-027-632-13961
7	61.2	45.3	818	13	US-10-027-632-150959
8	61.2	45.3	818	13	US-10-027-632-150960
9	50.6	37.5	603	13	US-10-027-632-135532
10	50.6	37.5	603	13	US-10-027-632-135520
11	48.4	35.9	871	13	US-10-027-632-134840
12	41.6	30.8	118067	15	US-10-081-327-32
13	40.2	29.8	322	13	US-10-027-632-272410
14	38.6	28.6	2126	12	US-10-325-107-59
15	37.6	27.9	9399	9	US-09-842-552-100
16	37.6	27.9	9399	9	US-09-842-552-102

17	37.4	27.7	5048	11	US-09-884-465A-2	Sequence 2, Appli
18	36.2	26.8	740	10	US-09-070-927A-846	Sequence 846, App
19	36	26.7	440	9	US-09-864-761-10165	Sequence 10165, A
20	35.8	26.5	400	8	US-08-781-986A-3707	Sequence 3707, Ap
21	35.6	26.4	9425	8	US-08-781-986A-87	Sequence 87, Appl
22	35	25.9	400	8	US-08-781-986A-3777	Sequence 3777, Ap
23	34.8	25.8	400	8	US-08-781-986A-3809	Sequence 3809, Ap
24	34.8	25.8	6591	8	US-08-781-986A-3114	Sequence 3114, Ap
25	34.4	25.5	214	9	US-09-815-242-3628	Sequence 3628, Ap
26	34.4	25.5	400	8	US-08-781-986A-3650	Sequence 3650, Ap
27	34.4	25.5	400	8	US-08-781-986A-3736	Sequence 3736, Ap
28	34.4	25.5	449	8	US-08-781-986A-3687	Sequence 3687, Ap
29	34.4	25.5	619	8	US-08-781-986A-3571	Sequence 3571, Ap
30	34	25.2	687	8	US-08-781-986A-608	Sequence 608, App
31	33	24.4	3309400	10	US-09-738-626-1	Sequence 1, Appli
32	32.2	23.9	11103	12	US-10-056-405-23	Sequence 23, Appl
33	32.2	23.9	11103	14	US-10-094-240-23	Sequence 23, Appl
34	31.2	23.1	7690	12	US-10-311-455-1096	Sequence 1096, Ap
35	30.4	22.5	9025608	14	US-10-156-761-1	Sequence 1, Appli
36	29.6	21.9	4792	10	US-09-863-040-5	Sequence 5, Appli
37	28.8	21.3	816	14	US-10-156-761-6550	Sequence 5, Appli
38	28.8	21.3	9025608	14	US-10-156-761-1	Sequence 1, Appli
39	28.4	21.0	585	10	US-09-954-973-3	Sequence 3, Appli
40	28.4	21.0	611	13	US-10-027-632-199163	Sequence 199163,
41	28.4	21.0	611	13	US-10-027-632-199164	Sequence 199164,
42	28.2	20.9	43804	9	US-09-970-711-1	Sequence 1, Appli
43	27.6	20.4	786	14	US-10-156-761-5266	Sequence 5266, Ap
44	27.6	20.4	1058	13	US-10-027-632-251155	Sequence 251155,
45	27.6	20.4	1058	13	US-10-027-632-251156	Sequence 251156,

#### ALIGNMENTS

#### RESULT 1

US-09-974-974-5  
; Sequence 5, Application US/09974974  
; Publication No. US20030013095A1  
; GENERAL INFORMATION:  
; APPLICANT: Kazunari TAIRA  
; APPLICANT: Masashi WARASHINA  
; APPLICANT: TOMOKO WARASHINA  
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a  
; TITLE OF INVENTION: target RNA by recognizing another molecule  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/974,974  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: JP 2000-313320  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 88  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal promoter sequence  
US-09-974-974-5

Query Match 61.3%; Score 82.8; DB 11; Length 88;  
Best Local Similarity 97.7%; Pred. No. 5.3e-20;  
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGUGUGUAGUGGUUACGUCGUAACGCGAAAGGUGCCCGG 60

Db 1 ACCGUGGUUCCGUGUGUAGUGGUUACGUCGUAACGCGAAAGGUGCCCGG 60

QY 61 UUGGAAACCGGCACUACAAACACAA 86

Db 61 UUGGAAACCGGCACUACAAACACAA 86

#### RESULT 2

Sat Sep 13 18:35:15 2003

us-09-763-590-1.rni

Page 9

Search completed: September 13, 2003, 08:05:55  
Job time : 67.4891 secs

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; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 947:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1586RP
;
US-08-998-416-947

Query Match 23.4%; Score 31.6; DB 3; Length 702;
Best Local Similarity 47.1%; Pred. No. 0.062;
Matches 33; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 4 GUUGUUUCCGAGUGAGUGGUAUCACGUGCCUAACGCGAAAGGUCGCCCGGUUC 63
Db 529 GTTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTC 470

QY 64 GAAACCGGGC 73
Db 469 GATCCTGGGC 460

RESULT 14
US-07-789-915A-7/c
; Sequence 7, Application US/07789915A
; Patent No. 5212058
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07789,915A
; FILING DATE: 19911108
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-5091AA
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4887 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1278..4013

US-08-998-416-947

Query Match 23.4%; Score 31.6; DB 3; Length 702;
Best Local Similarity 47.1%; Pred. No. 0.062;
Matches 33; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 4 GUUGUUUCCGAGUGAGUGGUAUCACGUGCCUAACGCGAAAGGUCGCCCGGUUC 63
Db 529 GTTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTC 470

QY 64 GAAACCGGGC 73
Db 469 GATCCTGGGC 460

RESULT 15
US-08-005-002C-7/c
; Sequence 7, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/005,002C
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,915
; FILING DATE: 08-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: MIT-5091AAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0558
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4887 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1278..4013

US-08-005-002C-7

Query Match 22.7%; Score 30.6; DB 1; Length 4887;
Best Local Similarity 46.4%; Pred. No. 0.27;
Matches 32; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 5 UUGGUUCCGAGUGAGUGGUAUCACGUGCCUAACGCGAAAGGUCGCCCGGUUCG 64
Db 4247 TTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTCG 4188

QY 65 AAACCGGGC 73
Db 4187 ATCCTGGGC 4179

US-07-789-915A-7

Query Match 22.7%; Score 30.6; DB 1; Length 4887;
Best Local Similarity 46.4%; Pred. No. 0.27;
Matches 32; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 5 UUGGUUCCGAGUGAGUGGUAUCACGUGCCUAACGCGAAAGGUCGCCCGGUUCG 64
Db 4247 TTGGTTTCGGTCTAGTCGGTTATGCGATCTGCTTAACACGAGAACGTCGCCAGTTCG 4188

QY 65 AAACCGGGC 73
Db 4187 ATCCTGGGC 4179
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; LOCATION: (405001)..(420000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (420001)..(435000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (435001)..(450000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (465001)..(480000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (480001)..(495000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (510001)..(525000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (525001)..(540000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (540001)..(555000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (555001)..(570000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (570001)..(585000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (585001)..(600000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (600001)..(615000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (615001)..(630000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (630001)..(645000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (645001)..(660000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (660001)..(675000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (675001)..(690000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (690001)..(705000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (705001)..(720000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (720001)..(735000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (735001)..(750000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (750001)..(765000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (765001)..(780000)

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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (780001)..(795000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (795001)..(810000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (810001)..(825000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (825001)..(840000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc.feature

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Query Match 24.1%; Score 32.6; DB 4; Length 1230025;  
 Best Local Similarity 54.5%; Pred. NO. 0.36;  
 Matches 30; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

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Qy 15 UAGUGUAGUGGUUACACGUCGUAACACGCGAAAGGUGCCCGUUGGAAACC 69
Db 209611 TAGAGTAGTGGTCATCTCGTGGCTCATACCAAGGTCGAGGTGCAATCC 209665

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## RESULT 13

```

US-08-998-416-947/c
; Sequence 947, Application US/089998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512.861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293.520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337.608
; FILING DATE: No. 614686member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-6

Query Match 29.5%; Score 39.8; DB 3; Length 171;
Best Local Similarity 86.3%; Pred. No. 4.6e-05;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACGCGGAAACGGU 132
Db 86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACGCGGAAACGGU 136

RESULT 7
US-08-512-861A-10
; Sequence 10, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512.861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293.520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337.608
; FILING DATE: No. 614686member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-4

Query Match 28.4%; Score 38.4; DB 3; Length 146;
Best Local Similarity 97.5%; Pred. No. 0.00014;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACG 121
Db 86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACG 125

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; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-10

Query Match 29.5%; Score 39.8; DB 3; Length 171;
Best Local Similarity 86.3%; Pred. No. 4.6e-05;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACGCGGAAACGGU 132
Db 86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACGCGGAAACGGU 136

RESULT 8
US-08-512-861A-4
; Sequence 4, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512.861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293.520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337.608
; FILING DATE: No. 614686member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-4

Query Match 28.4%; Score 38.4; DB 3; Length 146;
Best Local Similarity 97.5%; Pred. No. 0.00014;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 82 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACG 121
Db 86 CACACACUGAUGAGGACCGAAAGUCCGAAACGGGCACG 125

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Query Match 51.7%; Score 69.8; DB 3; Length 132;  
 Best Local Similarity 72.6%; Pred. No. 9.4e-16;  
 Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUUGUAGUGUUAUACGUCGUAACGCGGAAAGGUCGCCGG 60  
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||  
 Db 11 ACCGTGGTTCCTAGTGTAGTGTATCAGTTCGCTCACACGCGGACGGTCCCGG 70  
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||  
 QY 61 UUCGAAACCGGC 73  
 ::|||:|||||  
 Db 71 TTCGAAACCGGC 83  
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RESULT 4  
 PCT-US94-05700-17  
 ; Sequence 17, Application PC/TUS9405700  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
 ; TITLE OF INVENTION: RIBOZYME GENE THERAPY FOR HIV INFECTION AND AIDS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ROBBINS, BERLINER & CARSON  
 ; STREET: 201 NORTH FIGUEROA STREET  
 ; CITY: LOS ANGELES  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 90012  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/05700  
 ; FILING DATE: 17 MAY 1994  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BERLINER, ROBERT  
 ; REGISTRATION NUMBER: 20,121  
 ; REFERENCE/DOCKET NUMBER: 5555-209  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 213-977-1001  
 ; TELEFAX: 213-977-1003  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 133 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 97  
 ; OTHER INFORMATION: /note= "w" = INTERNAL NUCLEOTIDE  
 ; OTHER INFORMATION: SEQUENCE"  
 PCT-US94-05700-17

Query Match 51.7%; Score 69.8; DB 5; Length 133;  
 Best Local Similarity 72.6%; Pred. No. 9.4e-16;  
 Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUUGUAGUGUUAUACGUCGUAACGCGGAAAGGUCGCCGG 60  
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 Db 11 ACCGTGGTTCCTAGTGTAGTGTATCAGTTCGCTCACACGCGGACGGTCCCGG 70  
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||  
 QY 61 UUCGAAACCGGC 73  
 ::|||:|||||  
 Db 71 TTCGAAACCGGC 83  
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RESULT 5  
 US-08-512-861A-14  
 ; Sequence 14, Application US/08512861A

Patent No. 6146886  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James D. Thompson  
 ; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED  
 ; EXPRESSION OF THERAPEUTIC RNAs  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/512,861A  
 ; FILING DATE: August 8, 1995  
 ; PRIOR APPLICATION DATA: Two  
 ; APPLICATION NUMBER: 08/293,520  
 ; FILING DATE: August 19, 1994  
 ; APPLICATION NUMBER: 08/337,608  
 ; FILING DATE: No. 6146886ember 10, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 215/154  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 167  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-512-861A-14

Query Match 31.9%; Score 43; DB 3; Length 167;  
 Best Local Similarity 90.2%; Pred. No. 3.4e-06;  
 Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 78 CAAACACACACUGAGGAGCGACGAAAGGCGGAAAGGCGGCGGCGGAAA 128  
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 Db 101 CAAACACACACUGAGGAGCGACGAAAGGCGGAAAGGCGGCGGCGGAAA 151  
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RESULT 6  
 US-08-512-861A-6  
 ; Sequence 6, Application US/08512861A  
 ; Patent No. 6146886  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James D. Thompson  
 ; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED  
 ; EXPRESSION OF THERAPEUTIC RNAs  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage

OTHER INFORMATION: /note= "insertion location of  
foreign gene in pol III  
OTHER INFORMATION: transcription cassette in  
OTHER INFORMATION: vector pMT"  
US-08-245-742A-17

Query Match 51.7%; Score 69.8; DB 1; Length 132;  
Best Local Similarity 72.6%; Pred. No. 9.4e-16;  
Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUUGCCGAGUGGUGUUAUCACGUGGCUAACACGGGAAAGGUCGCCGG 60

DB 11 ACCGTGGTTCCGAGTAGTGTTATCAGTTCGCTCACACGGGAGCGGTCCCGG 70

QY 61 UUCGAAACGGGC 73

DB 71 TTCGAAACGGGC 83

## RESULT 2

US-08-465-483-17

Sequence 17, Application US/08465483

Patent No. 5811275

GENERAL INFORMATION:

APPLICANT: Wong-Staal, Flossie

APPLICANT: Yu, Mang

APPLICANT: Yamada, Osamu

APPLICANT: Ojwang, Joshua O.

APPLICANT: Leavitt, Mark

APPLICANT: Ho, Anthony

TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection

TITLE OF INVENTION: and AIDS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Tower

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,483

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: US 08/062,465

FILING DATE: 17-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/245,742

FILING DATE: 17-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 2307E-567-11

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: (96^97)

OTHER INFORMATION: /note= "insertion location of

OTHER INFORMATION: foreign gene in pol III  
OTHER INFORMATION: transcription cassette in  
OTHER INFORMATION: vector pMT"  
US-08-465-483-17

Query Match 51.7%; Score 69.8; DB 1; Length 132;

Best Local Similarity 72.6%; Pred. No. 9.4e-16;

Matches 53; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGGUGUUGCCGAGUGGUGUUAUCACGUGGCUAACACGGGAAAGGUCGCCGG 60

DB 11 ACCGTGGTTCCGAGTAGTGTTATCAGTTCGCTCACACGGGAGCGGTCCCGG 70

QY 61 UUCGAAACGGGC 73

DB 71 TTCGAAACGGGC 83

## RESULT 3

US-08-876-996-17

Sequence 17, Application US/08876996

Patent No. 6132962

GENERAL INFORMATION:

APPLICANT: Wong-Staal, Flossie

APPLICANT: Yu, Mang

APPLICANT: Yamada, Osamu

APPLICANT: Ojwang, Joshua O.

APPLICANT: Leavitt, Mark

APPLICANT: Ho, Anthony

TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection

TITLE OF INVENTION: and AIDS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Tower

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/876,996

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,742

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 2307E-567-10

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: (96^97)

OTHER INFORMATION: /note= "insertion location of

foreign gene in pol III

OTHER INFORMATION: transcription cassette in

OTHER INFORMATION: vector pMT"

US-08-876-996-17

GenCore version 5.1.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 07:56:11 ; Search time 45.4891 Seconds  
(without alignments)  
1309.911 Million cell updates/sec

Title: US-09-763-590-1

Perfect score: 135

Sequence: 1 accguugnuccgagugu.....ggcagcugcgaaacgguuuu 135

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	69.8	51.7	132	1	US-08-465-483-17
3	69.8	51.7	132	3	US-08-876-996-17
4	69.8	51.7	133	5	PCT-US94-05700-17
5	43	31.9	137	3	US-08-512-861A-14
6	39.8	29.5	171	3	US-08-512-861A-6
7	39.8	29.5	171	3	US-08-512-861A-10
8	38.4	28.4	146	3	US-08-512-861A-4
9	38.4	28.4	146	3	US-08-512-861A-8
10	34.4	25.5	186	4	US-09-107-532A-488
11	34.4	25.5	1483	1	US-08-270-076A-2
12	32.6	24.1	1230025	4	US-09-198-452A-1
13	31.6	23.4	782	3	US-08-998-416-947
14	30.6	22.7	4887	1	US-07-789-915A-7
15	30.6	22.7	4887	1	US-08-005-002C-7
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17	29.8	22.1	1664976	4	US-08-916-421B-1
18	29.6	21.9	648	3	US-08-998-416-111
19	29.6	21.9	4792	3	US-09-189-462-5
20	29.4	21.8	729	3	US-08-998-416-607
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22	28.8	21.3	1284	4	US-09-252-991A-6826
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24	28.6	21.2	1230025	4	US-09-198-452A-1
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28	20.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
29	27.4	20.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
30	27.4	20.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
31	27.2	20.1	5109	4	US-08-930-055A-2	Sequence 2, Appli
32	27	20.0	61663	4	US-08-453-702B-62	Sequence 62, Appli
33	26.6	19.7	724	1	US-08-599-252-98	Sequence 98, Appli
34	26.6	19.7	724	5	PCT-US96-06352-98	Sequence 98, Appli
35	26.6	19.7	724	5	PCT-US96-06583-98	Sequence 98, Appli
36	26.2	19.4	189	4	US-09-328-352-1239	Sequence 1239, Ap
37	26.2	19.4	724	3	US-08-961-083-45	Sequence 45, Appli
38	26.2	19.4	724	4	US-09-536-784-45	Sequence 45, Appli
39	26.2	19.4	16593	4	US-08-961-527-52	Sequence 52, Appli
40	26	19.3	34063	4	US-09-453-702B-96	Sequence 96, Appli
41	26	19.3	49795	4	US-09-453-702B-60	Sequence 60, Appli
42	25.8	19.1	2271	4	US-09-438-268-3	Sequence 3, Appli
43	25.8	19.1	49272	1	US-08-614-770A-1	Sequence 1, Appli
44	25.6	19.0	36	1	US-08-271-880A-224	Sequence 224, App
45	25.6	19.0	36	2	US-08-910-408-224	Sequence 224, App

## ALIGNMENTS

RESULT 1  
US-08-245-742A-17  
; Sequence 17, Application US/08245742A  
; Patent No. 5670361  
; GENERAL INFORMATION:  
; APPLICANT: Wong-Staal, Flossie  
; APPLICANT: Yu, Mang  
; APPLICANT: Yamada, Osamu  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Leavitt, Mark  
; APPLICANT: Ho, Anthony  
; TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection  
; TITLE OF INVENTION: and AIDS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/245,742A  
FILING DATE: 17-MAY-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/062,465  
FILING DATE: 17-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 2307E-567-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: (96-97)  
LOCATION:

COMMENT OS Artificial Sequence  
 PN JP 2001190282-A/11  
 PD 17-JUL-2001  
 PF 02-NOV-2000 JP 2000336082  
 PI KAZUNARI TAJRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI PI  
 KAWASAKI  
 PC  
 C12N15/09,A61K31/7105,A61K31/711,A61K38/00,A61K48/00,A61P31/12, PC  
 A61P43/00,  
 PC C12N9/22,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00, PC  
 A61K37/02  
 CC Description of Artificial Sequence: the sequence encoding CC  
 tRNAval-TAR GUU  
 CC Rz-CTE  
 CC Other information: the sequence of nucleotide numbers 1-91 is  
 CC of tRNAval  
 CC with 3'-modification  
 CC Other information: the sequence of nucleotide numbers 92-131  
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 CC Rz  
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 CC KpnI-recognition site  
 CC Other information: the sequence of nucleotide numbers 138-309  
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 CC is of an  
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 CC Other information: the sequence of nucleotide numbers 316-320  
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 CC terminator  
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 FT Location/Qualifiers

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 QY 61 UUCGAACCGGGGCACACACACACACACACUGAGGAC 99  
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Search completed: September 13, 2003, 10:39:38  
 Job time : 1378.46 secs



RESULT 10  
 LOCUS BD143601 137 bp RNA linear PAT 17-JAN-2003  
 DEFINITION Method of selecting high-function nucleic acid molecule in cell.  
 ACCESSION BD143601  
 VERSION BD143601.1 GI:27849359  
 KEYWORDS JP 2002125685-A/2.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 137)  
 AUTHORS Taira, K. and Sano, M.  
 TITLE Method of selecting high-function nucleic acid molecule in cell  
 JOURNAL Patent: JP 2002125685-A 2 08-MAY-2002;  
 DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL  
 SCIENCE AND HIROSHI YATSUSHI, TECHNOLOGY, KAZUNARI TAIRA  
 OS Artificial Sequence  
 COMMENT PN JP 2002125685-A/2  
 PD 08-MAY-2002  
 PF 30-OCT-2000 JP 2000331347  
 PI KAZUNARI TAIRA, MASAYUKI SANO  
 PC C12N15/09, C12N9/00, C12Q1/02, C12Q1/25, C12Q1/68, C12M15/00 CC  
 Description of Artificial Sequence: Sequence of tRNA-Luc GUA CC  
 Rz  
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 FT source 1..137

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 /db\_xref="taxon:32630"

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Query Match 63.3%; Score 85.4; DB 6; Length 137;  
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 Matches 79; Conservative 25; Mismatches 31; Indels 0; Gaps 0;  
 QY 1 ACCGUGUGUCCGAGUGUGUUAUCACGUGUCCUAACACGCGGAAAGGUCGCCGG 60  
 Db 1 ACCGTGTTCCGTAGTGTATCATCGTTCGCTAACACGCGGAAAGGTCGCCGG 60  
 QY 61 UUCGAAACCGGCGACUACACACACACUGAUGAGGACCGAAGGUCGCGAAGCGGCAC 120  
 Db 61 TTCGAAACCGGCGACUACACACACACUGAUGAGGACCGAAGGUCGCGAAGCGGCAC 120  
 QY 121 GUCGGAACCGGUU 135  
 Db 121 AACGTGATGTTT 135

RESULT 11  
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 DEFINITION Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex  
 ACCESSION AB080619  
 VERSION AB080619.1 GI:22531652  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Tachi, C., Nakamura, K., Horii, T., Murata, C., Nishimura, S.,  
 Nishino, K., Nakayama, A. and Taira, K.  
 TITLE Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 153)  
 AUTHORS Tachi, C.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of  
 Veterinary Medicine, Lab. Developmental and Reproductive

Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan  
 (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)  
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 /note="derived from tRNA"  
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 Matches 81; Conservative 22; Mismatches 30; Indels 0; Gaps 0;  
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 Db 1 ACCGTGTTCCGTAGTGTATCATCGTTCGCTAACACGCGGAAAGGTCGCCGG 60  
 QY 61 UUCGAAACCGGCGACUACACACACACUGAUGAGGACCGAAGGUCGCGAAGCGGCAC 120  
 Db 61 TTCGAAACCGGCGACUACACACACACUGAUGAGGACCGAAGGUCGCGAAGCGGCAC 120  
 QY 121 GUCGGAACCGGUU 133  
 Db 121 AAGCAACTGGGT 133

RESULT 12  
 LOCUS AX138449 151 bp DNA linear PAT 30-MAY-2001  
 DEFINITION Sequence 10 from Patent EPI097993.  
 ACCESSION AX138449  
 VERSION AX138449.1 GI:14274345  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Taira, K., Warashina, M., Kuwabara, T. and Kawasaki, H.  
 TITLE Functional ribozyme chimeric molecules capable of sliding  
 JOURNAL Patent: EP 1097993-A 10 09-MAY-2001;  
 Secretary of Agency of Industrial Science and Technology (JP);  
 Taira, Kazunari (JP)

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 Rz-Other information: the sequence of nucleotide numbers 92-131 is  
 1-91 is of tRNAval with 3'-modification. Other  
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 of TAR GUU Rz. Other information: the sequence of  
 nucleotide numbers 132-137 is of a KpnI-recognition  
 site. Other information: the sequence of nucleotide  
 numbers 138-140 is of a linker. Other information: the  
 sequence of nucleotide numbers 141-146 is of an  
 EcoRV-recognition site. Other information: the sequence of  
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 BASE COUNT 38 a 39 c 38 g 36 t  
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Query Match 62.7%; Score 84.6; DB 6; Length 151;  
 Best Local Similarity 69.7%; Pred. No. 7.5e-15;  
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BD015660  
LOCUS Slidable functional chimeric molecule. 142 bp RNA linear PAT 27-AUG-2002  
DEFINITION  
ACCESSION BD015660  
VERSION BD015660.1 GI:22556797  
KEYWORDS JP 2001190282-A/53.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 142)  
AUTHORS Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.  
TITLE Slidable functional chimeric molecule  
JOURNAL Patent: JP 2001190282-A 53 17-JUL-2001;  
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL  
SCIENCE AND MANABU NAKAJIMA TECHNOLOGY, KAZUNARI TAIRA  
OS Artificial Sequence  
PN JP 2001190282-A/53  
PD 17-JUL-2001  
PF 02-NOV-2000 JP 2000336082  
PI KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI PI  
KAWASAKI  
PC C12N15/09,A61K31/7105,A61K31/711,A61K38/00,A61K48/00,A61P31/12,PC  
A61P43/00,  
PC C12N9/22,C1201/02,C1201/68,G01N33/53,G01N33/566,C12N15/00,PC  
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Best Local Similarity 62.8%; Pred. No. 1.1e-15;  
Matches 81; Conservative 22; Mismatches 26; Indels 0; Gaps 0;  
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Db 1 ACCGTTGGTTCCGAGTGTAGTGTATCAGTTCGCTACACGCGGAAAGGTCGCGG 60  
QY 61 UUGGAAACCGGCGACUACAAACACACACUGAUGAGGACCGGAAAGGUCGCGGAC 120  
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QY 121 GUGGGAAC 129  
Db 121 GCGCGAAC 129  
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E33214/c 109 bp DNA linear PAT 31-JAN-2002  
LOCUS Expression system for functional nucleic acid transcription.  
DEFINITION  
ACCESSION E33214  
VERSION E33214.1 GI:18624008  
KEYWORDS JP 2000069972-A/12.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 109)  
AUTHORS Tabira,K., Okawa,A. and Ozeki,S.  
TITLE Expression system for functional nucleic acid transcription  
JOURNAL Patent: JP 2000069972-A 12 07-MAR-2000;  
AGENCY OF IND SCIENCE & TECHNOL  
OS Artificial Sequence

PN JP 2000069972-A/12  
PD 07-MAR-2000  
PF 31-AUG-1998 JP 1998244755  
PR KAZUNARI TAIRA,ATSUSHI OKAWA,SHIORI OZEKI  
PI C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00,CC  
PC C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00,CC  
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Best Local Similarity 86.2%; Pred. No. 4.3e-15;  
Matches 75; Conservative 11; Mismatches 1; Indels 0; Gaps 0;  
QY 49 AAAGGUGGCGGUGUAGGAAACCGGCGGACUACAAACACACACUGAUGAGGACCGGAAAGGUC 108  
Db 109 AAAGTTCGCGGTTTCGAAACCGGCGGCACTACAAACACACACTGATGAGGACCGGAAAGGAC 50  
QY 109 CGAAACGGGCGACGUGCGGAAACGGUUU 135  
Db 49 CGAAACGGGCGACGTCGGAACGGTTTT 23  
RESULT 9  
AX429079 137 bp mRNA linear PAT 21-JUN-2002  
LOCUS Sequence 2 from Patent EP1201751.  
DEFINITION  
ACCESSION AX429079  
VERSION AX429079.1 GI:21540419  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Taira,K. and Sano,M.  
TITLE Method for selecting highly functional nucleic acid molecules  
within cells  
JOURNAL Patent: EP 1201751-A 2 02-MAY-2002;  
National Institute of Advanced Industrial Science and Technology  
(JP)  
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Best Local Similarity 58.5%; Pred. No. 4.3e-15;  
Matches 79; Conservative 25; Mismatches 31; Indels 0; Gaps 0;  
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Db 1 ACCGTTGGTTCCGAGTGTAGTGTATCAGTTCGCTACACGCGGAAAGGTCGCGG 60  
QY 61 UUGGAAACCGGCGACUACAAACACACACUGAUGAGGACCGGAAAGGUCGCGGAC 120  
Db 61 TTGGAACCGGCGGCACTACAAACCACTTTATTCGCGGCTGATGAGGCGGAAAGGCGGA 120  
QY 121 GUGGGAACGGUUU 135  
Db 121 AACGTGATGTTTTT 135

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VERSION      BD174679.1  GI:29120369
KEYWORDS     JP 2002262880-A/5
SOURCE       synthetic construct
ORGANISM     synthetic construct
REFERENCE    1 (bases 1 to 175)
AUTHORS      Takebe,Y. and Okawa,J.
TITLE        Ribozyme expression system
JOURNAL      Patent: JP 2002262880-A 5 17-SEP-2002;
              DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
              YUTAKA TAKEBE, JUN OKAWA
COMMENT      OS Artificial Sequence
              PN JP 2002262880-A/5
              PD 17-SEP-2002
              PF 09-MAR-2001 JP 2001067253
              PI YUTAKA TAKEBE, JUN OKAWA
              PC C12N15/09,A61K31/711,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
              PC C12N5/00,
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              CC expressing cassette of the invention
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QY 111 AACCGGGCACGUCGGAACCGGUU 135
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Db 149 AACACTTGATTCGCGAAACGGTTT 173

RESULT 5
LOCUS      AB080624
DEFINITION Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
VERSION    AB080624
KEYWORDS   anti-mSryRNA/Rz6.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
           Nishino,K., Nakayama,A. and Taira,K.
TITLE      Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 153)
AUTHORS    Tachi,C.
TITLE      Direct Submission
JOURNAL    Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
           Veterinary Medicine, Lab. Developmental and Reproductive
           Biotechnology; 1-17-71, Fuchinobe, Sagamihara-shi 229-8501, Japan

FEATURES
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           (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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RESULT 6
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VERSION    AX138492
KEYWORDS   AX138492.1 GI:14274388
SOURCE     synthetic construct
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           artificial sequences.
REFERENCE  1
AUTHORS    Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
TITLE      Functional ribozyme chimeric molecules capable of sliding
JOURNAL    Patent: EP 1097993-A 53 09-MAY-2001;
           Secretary of Agency of Industrial Science and Technology (JP) ;
           Taira, Kazunari (JP)
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               Matches 81; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

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OS	Artificial Sequence				
PN	JP 2000069972-A/1				
PD	07-MAR-2000				
PF	31-AUG-1998 JP 1998244755				
PR					
PI	KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI				
PC	C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC				
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Ddb	1	ACCGTTGGTTCCTAGTAGTGATCATCAGTTCGCCTACACGCGAAGGTCCCCGG	60		
QY	61	UUCGAAACCGGGCACURACACACACACATGATGAGGACCGAAGGUCGGAACGGCAC	120		
Ddb	61	TTCGAAACCGGGCACTAACACAACACTGATGAGGACCGAAGGTCCTCGAAGCGGCAC	120		
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LOCUS	E33204	142 bp	RNA	linear	PAT 31-JAN-2002
DEFINITION	Expression system for functional nucleic acid transcription.				
ACCESSION	E33204				
VERSION	E33204.1	GI:18623998			
KEYWORDS	JP 2000069972-A/2.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	artificial sequences.				
AUTHORS	1. (bases 1 to 142)				
TITLE	Tabira,K., Okawa,A. and Ozeki,S.				
JOURNAL	Expression system for functional nucleic acid transcription				
COMMENT	Patent: JP 2000069972-A 2 07-MAR-2000; AGENCY OF IND SCIENCE & TECHNOL OS JP 2000069972-A/2 PN JP 2000069972-A/2 PD 07-MAR-2000 PF 31-AUG-1998 JP 1998244755				
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PI	KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI				
PC	C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC				
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Db	61	TTG	GAACCGGGCACTACAAACCAACACACACACACTGATGAGGACCGGAAGGTCCGGAAC	120
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DEFINITION	BD174680			
ACCESSION	BD174680			
VERSION	BD174680.1	GI:29120370		
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ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 175)			
AUTHORS	Takebe, Y. and Okawa, J.			
TITLE	Ribozyme expression system			
JOURNAL	Patent: JP 2002262880-A 6 17-SEP-2002;			
	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF			
	YUTAKA TAKEBE, JUN OKAWA			
COMMENT	OS Artificial Sequence			
	PN JP 2002262880-A/6			
	PD 17-SEP-2002			
	PF 09-MAR-2001 JP 2001067253			
	PI YUTAKA TAKEBE, JUN OKAWA			
	PC C12N15/09, A61K31/711, A61K35/76, A61K48/00, A61P31/18, C12N5/10,			
	PC C12N9/00,			
	PC C12N15/00, C12N5/00			
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Db	89	TCG	GAACCGGGCACTACNAACCAACCGCATAGATGCTGATGAGGACCGGAAGGTCCG	148
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DEFINITION	BD174679			
ACCESSION	BD174679			
LOCUS	BD174679			
DEFINITION	BD174679			
ACCESSION	BD174679			

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 09:38:16 : Search time 1374.46 Seconds  
(without alignments)  
4018.170 Million cell updates/sec

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: gb\_ro.\*

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12: gb\_sy.\*

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14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

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18: em\_in.\*

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20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

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27: em\_sts.\*

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29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

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35: em\_htg\_rod.\*

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37: em\_htg\_vrt.\*

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40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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6	87.4	64.7	142	6	AX138492	AX138492 Sequence
7	87.4	64.7	142	6	BD015660	BD015660 Slidable
8	85.4	63.3	109	6	E33214	E33214 Expression
9	85.4	63.3	137	6	AX429079	AX429079 Sequence
10	85.4	63.3	137	6	BD143601	BD143601 Method of
11	85	63.0	153	12	AB080619	AB080619 Synthetic
12	84.6	62.7	151	6	AX138449	AX138449 Sequence
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14	84.6	62.7	320	6	AX138450	AX138450 Sequence
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17	83.8	62.1	153	12	AB080620	AB080620 Synthetic
18	83.8	62.1	153	12	AB080621	AB080621 Synthetic
19	83.8	62.1	153	12	AB080623	AB080623 Synthetic
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# ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
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E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
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E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
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E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
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E33203	E33203	Expression system for functional nucleic acid transcription.	E33203	E33203.1	GI:18623997	synthetic construct	artificial construct	1 (bases 1 to 136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;
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XX 09-MAR-2001; 2001JP-0067253.
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XX PA
XX (TAKE/) TAKEBE Y.
XX PA
XX (OKAW/) OKAWA J.
XX PS
XX WPI; 2003-132124/13.
XX DR
XX Ribozyme expression cassette, useful for preparing a cell insensitive
XX PT to HIV and for inhibiting growth of HIV, comprises a tetracyclin
XX PT operator, at least one promoter and a sequence encoding a ribozyme
XX PT successively from the upstream side -
XX PS
XX Claim 6; Page 15; 27pp; Japanese.
XX PS
XX The present invention relates to a ribozyme expression cassette
XX CC comprising a tetracyclin operator, at least one promoter and a DNA
XX CC sequence encoding a ribozyme successively from the 5' end. The
XX CC tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from
XX CC the transcription initiating site of the promoter. The expression
XX CC cassette is useful in a method for preparing a cell having no sensitivity
XX CC to HIV, and for inhibiting the growth of HIV. To illustrate the
XX CC invention, a tet 01-human tRNAVal promoter cassette was constructed,
XX CC using the present sequence.
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XX SQ
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DB 89 TTCGAAACCGGGCACATACAAACACCA 114
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XX 23-APR-2002.
XX PD
XX 13-OCT-2000; 2000JP-0313320.
XX PF
XX 13-OCT-2000; 2000JP-0313320.
XX PR
XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
XX PA
XX WPI; 2002-483792/52.
XX DR
XX A nucleic acid enzyme which has selective and effective eradicating
XX PT activity towards harmful cells by acquiring cleavage activity of a
XX PT specific target RNA by recognition of the other RNA molecule -
XX PT
XX Disclosure; Fig 7; 17pp; Japanese.
XX PS
XX The invention relates to a nucleic acid enzyme with modifiable RNA
XX CC cleavage activity. More specifically the invention relates to a nucleic
XX CC acid enzyme, trans maxizyme, which has selective and effective
XX CC eradicating activity towards harmful cells by acquiring cleavage activity
XX CC of a specific target RNA by recognition of the other RNA molecule. The
XX CC enzyme of the invention is useful for cleaving target RNA and is useful
XX CC in treating diseases caused by the target RNA. This polynucleotide
XX CC sequence represents the tRNA-val T-MzL sequence related to the maxizyme
XX CC enzyme of the invention.
XX SQ
Sequence 138 BP; 31 A; 38 C; 32 G; 37 U; 0 other;

```

```

Query Match 61.3%; Score 82.8; DB 24; Length 138;
Best Local Similarity 97.7%; Pred. No. 5.2e-19;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ACCGUUGGUUCCGUGAGUGGUUACGUCGUAACGCGAAGGUCGCCGG 60
DB 1 ACCGUUGGUUCCGUGAGUGGUUACGUCGUAACGCGAAGGUCGCCGG 60
QY 61 UUCGAAACCGGGCACUACAAACACAA 86
DB 61 UUCGAAACCGGGCACUACAAACACCA 86

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Search completed: September 13, 2003, 09:52:32  
Job time : 198.152 secs



PT disease, comprises region with binding affinity for molecule capable of  
 PT sliding -  
 XX Example 1; Page 13; 76pp; English.  
 XX The present sequence is that of a DNA cassette forming part of a  
 CC ribozyme expression vector of the invention. The cassette  
 CC comprises the human placental TRNAval promoter (see AAF90356), with  
 CC a 3' modification, a DNA sequence corresponding to HIV-1  
 CC mRNA-targeted ribozyme TAR GUD R2 (see AAF90354), and a 3'  
 CC constitutive transport element (CTE, see AAF90344) derived from  
 CC Mason-Pfizer monkey virus. Chimeric molecules of the invention  
 CC include ribozymes such as TAR GUD R2 linked to a CTE, and  
 CC expression vectors for such chimeric molecules. These are used in  
 CC a claimed method to prevent or treat viral diseases, diseases  
 CC associated with apoptosis or diseases associated with abnormal  
 CC gene expression. They are also used in a claimed method of  
 CC specifically cleaving a target nucleic acid, especially a viral  
 CC gene, protooncogene or a gene associated with apoptosis. Use  
 CC of the CTE facilitates cleavage of RNA previously considered  
 CC refractory because of local structure.  
 XX Sequence 320 BP; 93 A; 79 C; 81 G; 67 T; 0 other;  
 SQ Query Match 62.7%; Score 84.6; DB 22; Length 320;  
 Best Local Similarity 69.7%; Pred. No. 1.6e-19;  
 Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 ACCGUGGUGUUCGGUAGUGGUAUCACGUCGCUAACACGGCGAAAGGUCGCCGG 60  
 Db 1 ACCGTGTGTTCCGTAGTGTAGTGTATACGTTTCGCTAACACGGCGAAAGGTCGCCGG 60  
 QY 61 UUCGAAACCGGCGACUACAAACACACACACACUGAUGAGGAC 99  
 Db 61 TTCGAAACCGGCGACTACAAAACCACTTTATCTGTC 99  
 RESULT 10  
 AAL10600  
 ID AAL10600 standard; RNA; 88 BP.  
 XX AC AAZ10600;  
 XX 17-NOV-1999 (first entry)  
 XX Nucleotide sequence of tRNA-val.  
 XX Nucleic acid enzyme; maxizyme; allosteric RNA-cleaving activity;  
 KW RNA cleavage; chronic myeloid leukemia;  
 KW Philadelphia chromosome abnormality; ss.  
 XX Synthetic.  
 XX WO9946388-A1.  
 XX 16-SEP-1999.  
 XX 11-MAR-1999; 99WO-JP01187.  
 XX 12-MAR-1998; 98JP-0060969.  
 XX 30-OCT-1998; 98JP-0311098.  
 XX (TAIS ) TAISHO PHARM CO LTD.  
 PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
 XX Taira K, Kuwabara T, Hitoshio A;  
 XX WPI; 1999-551415/46.  
 XX Nucleic acid enzyme having allosteric RNA-cleaving activity, used for  
 PT treatment of chronic myeloid leukemia -  
 XX Claim 8; Page 55; 93pp; Japanese.

XX The specification describes nucleotide sequences which make up the  
 CC left and right arms of a nucleic acid enzyme (maxizyme). The maxizyme  
 CC has allosteric RNA-cleaving activity on a specific target RNA. The  
 CC maxizyme can be used for efficient cleavage of RNA molecules at  
 CC specific points, especially for the prevention and treatment of  
 CC chronic myeloid leukemia and Philadelphia chromosome abnormality.  
 CC The present sequence is used in the course of the invention.  
 XX Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;  
 SQ Query Match 61.3%; Score 82.8; DB 20; Length 88;  
 Best Local Similarity 97.7%; Pred. No. 4.6e-19;  
 Matches 84; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ACCGUGGUGUUCGGUAGUGGUAUCACGUCGCUAACACGGCGAAAGGUCGCCGG 60  
 Db 1 ACCGUGGUGUUCGGUAGUGGUAUCACGUCGCUAACACGGCGAAAGGUCGCCGG 60  
 QY 61 UUCGAAACCGGCGACUACAAACACAA 86  
 Db 61 UUCGAAACCGGCGACUACAAACAA 86  
 RESULT 11  
 AAL40450  
 ID AAL40450 standard; tRNA; 88 BP.  
 XX AC AAL40450;  
 XX 19-SEP-2002 (first entry)  
 XX Maxizyme related tRNA-val promoter sequence.  
 DE Enzyme; modifiable RNA cleavage activity; maxizyme-constituting RNA;  
 KW trans maxizyme; tRNA-val; ss.  
 XX Unidentified.  
 XX JP2002119283-A.  
 XX 23-APR-2002.  
 XX 13-OCT-2000; 2000JP-0313320.  
 XX 13-OCT-2000; 2000JP-0313320.  
 PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.  
 XX WPI; 2002-483792/52.  
 PT A nucleic acid enzyme which has selective and effective eradicating  
 PT activity towards harmful cells by acquiring cleavage activity of a  
 PT specific target RNA by recognition of the other RNA molecule -  
 XX Claim 12; Page 2; 17pp; Japanese.  
 XX The invention relates to a nucleic acid enzyme with modifiable RNA  
 CC cleavage activity. More specifically the invention relates to a nucleic  
 CC acid enzyme, trans maxizyme, which has selective and effective  
 CC eradicating activity towards harmful cells by acquiring cleavage activity  
 CC of a specific target RNA by recognition of the other RNA molecule. The  
 CC enzyme of the invention is useful for cleaving target RNA and is useful  
 CC in treating diseases caused by the target RNA. This polynucleotide  
 CC sequence represents the tRNA-val promoter sequence relating to the  
 CC maxizyme enzyme of the invention.  
 XX Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;  
 SQ Query Match 61.3%; Score 82.8; DB 24; Length 88;  
 Best Local Similarity 97.7%; Pred. No. 4.6e-19;  
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX Sequence 137 BP; 33 A; 34 C; 34 G; 36 U; 0 other;  
 SQ Query Match 63.3%; Score 85.4; DB 24; Length 137;  
 Best Local Similarity 77.0%; Pred. No. 6.5e-20;  
 Matches 104; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGUGAGUGGUGAUCAGUCCUACACGCGAAGGUGCCCGG 60  
 Db 1 ACCGUGUUCGUGAGUGGUGAUCAGUCCUACACGCGAAGGUGCCCGG 60  
 QY 61 UUCGAAACCGGCGACUACACACACACGAGGAGGUGCCGAAAGCGGCAC 120  
 Db 61 UUCGAAACCGGCGACUACACACACACGAGGAGGUGCCGAAAGCGGCAC 120  
 QY 121 GUCGGAACGUGUUU 135  
 Db 121 AACGUGAGUGUUUU 135

RESULT 8  
 AAF90357  
 ID AAF90357 standard; DNA; 151 BP.  
 XX AAF90357;  
 AC  
 XX 06-AUG-2001 (first entry)  
 DT  
 XX DNA cassette for tRNAval-linked ribozyme TAR GUU Rz.  
 DE  
 XX Ribozyme; constitutive transport element; virucide; gene therapy;  
 KW HIV-1; tRNAval; promoter; ss.  
 XX Chimeric - Homo sapiens.  
 OS Chimeric - synthetic.  
 XX

Key Location/Qualifiers  
 FT promoter 1..91  
 FT /tag= a  
 FT /note= "tRNAval with 3' modification"  
 FT misc\_feature 92..131  
 FT /tag= b  
 FT /note= "TAR GUU Rz"  
 FT terminator 147..151  
 FT /tag= c  
 FT EP1097993-A2.  
 XX  
 XX 09-MAY-2001.  
 XX 03-NOV-2000; 2000EP-0250368.  
 XX 05-NOV-1999; 99JP-0316133.  
 XX (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.  
 XX (TAIR/) TAIRA K.  
 XX Taira K, Warashina M, Kuwabara T, Kawasaki H;  
 XX WPI; 2001-357832/38.  
 XX Novel chimeric molecule useful for clarifying biological function of  
 PT target nucleic acid and for treating viral diseases, and Alzheimer's  
 PT disease, comprises region with binding affinity for molecule capable of  
 PT sliding -  
 XX  
 PS Example 1; Page 13; 76pp; English.  
 XX The present sequence is that of a DNA cassette forming part of a  
 CC ribozyme expression vector of the invention. The cassette  
 CC comprises the human placental tRNAval promoter (see AAF90356), with  
 CC a 3' modification, and a DNA sequence corresponding to HIV-1  
 CC mRNA-targeted ribozyme TAR GUU Rz (see AAF90354). Chimeric

CC molecules of the invention include ribozymes such as TAR GUU Rz  
 CC linked to a constitutive transport element (see AAF90344), and  
 CC expression vectors for such chimeric molecules. These are used in  
 CC a claimed method to prevent or treat viral diseases, diseases  
 CC associated with apoptosis or diseases associated with abnormal  
 CC gene expression. They are also used in a claimed method of  
 CC specifically cleaving a target nucleic acid, especially a viral  
 CC gene, protooncogene or a gene associated with apoptosis. Use  
 CC of the CRE facilitates cleavage of RNA previously considered  
 CC refractory because of local structure.  
 XX  
 SQ Sequence 151 BP; 38 A; 39 C; 38 G; 36 T; 0 other;  
 Query Match 62.7%; Score 84.6; DB 22; Length 151;  
 Best Local Similarity 69.7%; Pred. No. 1.3e-19;  
 Matches 69; Conservative 21; Mismatches 9; Indels 0; Gaps 0;

QY 1 ACGGUGGUGUUCGUGAGUGGUGAUCAGUCCUACACGCGAAGGUGCCCGG 60  
 Db 1 ACGGUGGUGUUCGUGAGUGGUGAUCAGUCCUACACGCGAAGGUGCCCGG 60  
 QY 61 UUCGAAACCGGCGACUACACACACACGAGGAGGUGCCGAAAGCGGCAC 99  
 Db 61 UUCGAAACCGGCGACUACACACACACGAGGAGGUGCCGAAAGCGGCAC 99

RESULT 9  
 AAF90358  
 ID AAF90358 standard; DNA; 320 BP.  
 XX AAF90358;  
 AC  
 XX 06-AUG-2001 (first entry)  
 DT  
 XX tRNAval-linked ribozyme TAR GUU Rz-CTE.  
 DE  
 XX Ribozyme; constitutive transport element; virucide; gene therapy;  
 KW HIV-1; tRNAval; promoter; ss.  
 XX Chimeric - Homo sapiens.  
 OS Chimeric - synthetic.  
 OS Chimeric - Simian mason-pfizer type d retrovirus.  
 XX

Key Location/Qualifiers  
 FT promoter 1..91  
 FT /tag= a  
 FT /note= "tRNAval with 3' modification"  
 FT misc\_feature 92..131  
 FT /tag= b  
 FT /note= "TAR GUU Rz"  
 FT misc\_feature 138..309  
 FT /tag= c  
 FT /note= "constitutive transport element"  
 FT terminator 316..320  
 FT /tag= d  
 XX EP1097993-A2.  
 XX  
 XX 09-MAY-2001.  
 XX 03-NOV-2000; 2000EP-0250368.  
 XX 05-NOV-1999; 99JP-0316133.  
 XX (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.  
 XX (TAIR/) TAIRA K.  
 XX Taira K, Warashina M, Kuwabara T, Kawasaki H;  
 XX WPI; 2001-357832/38.  
 XX Novel chimeric molecule useful for clarifying biological function of  
 PT target nucleic acid and for treating viral diseases, and Alzheimer's





```

XX ABZ21216;
XX AC
XX DT
XX DE
XX DE Nucleotide sequence of ribozyme expressing cassette, SEQ ID 5.
XX KW Antiviral; gene therapy; ribozyme expression cassette;
XX KW tetracyclin operator; promoter; ribozyme; anti-HIV; ds.
XX OS Synthetic.
XX PN JP2002262880-A.
XX PN 17-SEP-2002.
XX PD
XX PF
XX PR 09-MAR-2001; 2001JP-0067253.
XX PR 09-MAR-2001; 2001JP-0067253.
XX PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX PA (TAKE/) TAKEBE Y.
XX PA (OKAW/) OKAWA J.
XX DR
XX DR WPI; 2003-132124/13.
XX PT Ribozyme expression cassette, useful for preparing a cell insensitive
XX PT to HIV and for inhibiting growth of HIV, comprises a tetracyclin
XX PT operator, at least one promoter and a sequence encoding a ribozyme
XX PT successively from the upstream side -
XX PS
XX PS Disclosure; Page 16; 27pp; Japanese.
XX CC
XX CC The present invention relates to a ribozyme expression cassette
XX CC comprising a tetracyclin operator, at least one promoter and a DNA
XX CC sequence encoding a ribozyme successively from the 5' end. The
XX CC tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from
XX CC the transcription initiating site of the promoter. The expression
XX CC cassette is useful in a method for preparing a cell having no sensitivity
XX CC to HIV, and for inhibiting the growth of HIV. The present sequence was
XX CC used to illustrate the invention.
XX SQ
XX SQ Sequence 175 BP; 47 A; 39 C; 41 G; 48 T; 0 other;

Query Match 66.2%; Score 89.4; DB 25; Length 175;
Best Local Similarity 64.1%; Pred. No. 2.9e-21;
Matches 93; Conservative 26; Mismatches 16; Indels 10; Gaps 1;

Qy 1 ACCGUUGUUCGUGAGUGUGUUAUCACGUUCGCUAACACGCGAAAGUCCCGG 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 29 ACCGTTGGTTCCGTAGTGTAGTGTATACGTTCCCTAACACGCGAAAGTCCCGG 88
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Qy 61 UUGGAAACCGGGCACUACAAAC-----AACUGAGAGACCGAAAGUCCG 110
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 89 TTCGAAACCGGGCACACTACAAACACCAACGATTGCTGATGAGGACCGAAAGTCCG 148
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Qy 111 AAACGGCCACGUGCGGAACGGUUU 135
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 149 AAACACTGATTCCGGAAACGGTTT 173
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 5
AAAF90396
ID AAF90396 standard; RNA; 142 BP.
XX
XX AC AAF90396;
XX DT
XX DT 06-AUG-2001 (first entry)
XX DE
XX DE Mouse procaspase-3 mRNA targeted ribozyme CPP Rz5.
XX KW Ribozyme; constitutive transport element; mouse; procaspase-3;
XX KW CPP32; apoptosis; gene therapy; ss.

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```

XX OS Synthetic.
XX PN EPI097993-A2.
XX PD
XX PD 09-MAY-2001.
XX PF
XX PF 03-NOV-2000; 2000EP-0250368.
XX PR
XX PR 05-NOV-1999; 99JP-0316133.
XX PA (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
XX PA (TAIR/) TAIRA K.
XX PI Taira K, Warashina M, Kuwabara T, Kawasaki H;
XX DR WPI; 2001-357832/38.
XX PT Novel chimeric molecule useful for clarifying biological function of
XX PT target nucleic acid and for treating viral diseases, and Alzheimer's
XX PT disease, comprises region with binding affinity for molecule capable of
XX PT sliding -
XX PS
XX PS Example 1; Page 49; 76pp; English.
XX CC
XX CC The present sequence is that of novel ribozyme CPP Rz5, which is
XX CC targeted to a stem-structured site in mouse CPP32 mRNA that was
XX CC previously considered inaccessible. CPP32 is an apoptosis-related
XX CC gene encoding procaspase-3. CPP Rz5 was used to demonstrate the high
XX CC efficacy of hybrid ribozymes linked to a constitutive transport
XX CC element (CTE, See AAF30944) for inhibition gene expression.
XX CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see
XX CC AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme
XX CC expression plasmids and procaspase-3 expression levels were
XX CC determined by Western blotting after 36 hr. CTE-linked ribozymes
XX CC were more effective than their conventional counterparts for
XX CC inhibiting CPP32 gene expression. The CTE moiety facilitates
XX CC cleavage of RNA previously considered refractory because of local
XX CC high-order structure. It binds to RNA helicase A, which has
XX CC functions of binding to RNA, sliding and unwinding its high-order
XX CC structure. Chimeric molecules of the invention, including
XX CC CTE-ribozymes, and expression vectors, are used to prevent or
XX CC treat viral diseases, diseases associated with apoptosis or
XX CC diseases associated with abnormal gene expression (claimed). They
XX CC are also used in a claimed method of specifically cleaving a target
XX CC nucleic acid, especially a viral gene, protooncogene or a gene
XX CC associated with apoptosis.
XX SQ
XX SQ Sequence 142 BP; 39 A; 37 C; 37 G; 29 U; 0 other;

Query Match 64.7%; Score 87.4; DB 22; Length 142;
Best Local Similarity 79.8%; Pred. No. 1.3e-20;
Matches 103; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 ACCGUUGUUUCCGUGAGUGUGUUAUCACGUUCGCUAACACGCGAAAGUCCCGG 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 ACCGUUGUUUCCGUGAGUGUGUUAUCACGUUCGCUAACACGCGAAAGUCCCGG 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Qy 61 UUCGAAACCGGGCACUACAAACACACACUGAGAGACCGAAAGUCCCGGCGAC 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 UUCGAAACCGGGCACUACAAACACCAACUUCUUGAGAGCGGAGUCUGAGGCGCGAAA 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Qy 121 GUCCGAAAC 129
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 GUCCGAAAC 129
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 6
AAZ58601/c
ID AAZ58601 standard; DNA; 109 BP.
XX
XX AC AAZ58601;
XX XX

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GenCore version 5.1.16  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 08:06:21 ; Search time 195.652 Seconds  
(without alignments)  
1862.612 Million cell updates/sec

Title: US-09-763-590-1

Perfect score: 135

Sequence: 1 accgugguuuccgagugu.....ggcagcugcgaacgguuuu 135

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	100.0	136	21	AAZ58590 Nucleotide sequenc
2	119	88.1	142	21	AAZ58591 Nucleotide sequenc
3	91.2	67.6	175	25	ABZ21217 Nucleotide sequenc
4	89.4	66.2	175	25	ABZ21216 Nucleotide sequenc
5	87.4	64.7	142	22	AAF90396 Mouse procaspase-3
6	85.4	63.3	109	21	AAZ58601 Sequence of a lowe
7	85.4	63.3	137	24	ABZ51149 tRNA-Luc GUA Rz Ri
8	84.6	62.7	151	22	AAF90357 DNA cassette for t

9	84.6	62.7	320	22	AAF90358 tRNAVal-linked rib
10	82.8	61.3	88	20	AAZ10600 Nucleotide sequenc
11	82.8	61.3	88	24	AAZ10450 Nucleotide sequenc
12	82.8	61.3	88	25	ABX12785 Human RNA sequence
13	82.8	61.3	100	22	AAZ47825 Human tRNA promote
14	82.8	61.3	117	25	ABZ21212 tet 01-tRNAVal seq
15	82.8	61.3	138	24	AAZ40467 Maxizyme related t
16	82.8	61.3	141	22	AAF90395 Mouse procaspase-3
17	82.8	61.3	142	22	AAF90392 Mouse procaspase-3
18	82.8	61.3	142	22	AAF90393 Mouse procaspase-3
19	82.8	61.3	142	22	AAF90394 Mouse procaspase-3
20	78	57.8	128	21	AAZ58592 Nucleotide sequenc
c 21	74.2	55.0	325	17	AAZ58592 Plasmid pBTVI-434
c 22	74.2	55.0	332	17	AAZ58592 Plasmid pBTVI-434
c 23	74.2	55.0	406	17	AAZ58592 Plasmid pBTVI-434
c 24	74.2	55.0	406	17	AAZ58592 Plasmid pBTVI-434
c 25	73.4	54.4	149	21	AAZ58594 Nucleotide sequenc
26	73	54.1	95	21	AAZ58593 Nucleotide sequenc
27	73	54.1	95	22	AAF90356 Human placental tr
28	73	54.1	269	17	AAZ58593 Plasmid pBTVI-434
c 29	73	54.1	139904	24	AAZ58593 Human cDNA differe
30	69.8	51.7	132	18	AAZ58593 Pol III transcript
31	69.8	51.7	132	19	AAZ58593 Pol III transcript
32	69.8	51.7	132	22	AAZ58593 Cassette pMTJ. Sy
c 33	66.8	49.5	113	21	AAZ58596 Sequence of an ant
34	66	48.9	110	21	AAZ58595 Sequence of a sens
c 35	63.8	47.3	43226	20	AAZ58595 Nucleic acid sequ
36	54.4	40.3	2451	23	ABZ24834 Drosophila melanog
37	53.6	39.7	4669	23	ABZ24834 Drosophila melanog
c 38	53.4	39.6	2289	23	ABZ24836 Drosophila melanog
c 39	53.2	39.4	3886	23	ABZ24836 Drosophila melanog
c 40	53.2	39.4	22967	23	ABZ24836 Drosophila melanog
c 41	50	37.0	7799	23	ABZ24836 Drosophila melanog
c 42	50	37.0	7799	23	ABZ24836 Drosophila melanog
c 43	50	37.0	27433	23	ABZ24836 Drosophila melanog
c 44	47	34.8	106	21	AAZ58602 Sequence of a lowe
c 45	45	33.3	4034	23	ABZ24836 Drosophila melanog

## ALIGNMENTS

RESULT 1  
AAZ58590  
ID AAZ58590 standard; RNA; 136 BP.  
XX  
AC AAZ58590;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Nucleotide sequence of hammerhead ribozyme Rz2.  
XX  
KW Hammerhead ribozyme; antiviral; gene expression; ss.  
XX  
OS Synthetic.  
XX  
PN JP2990268-B1.  
XX  
PD 13-DEC-1999.  
XX  
PF 31-AUG-1998; 98JP-0244755.  
XX  
PR 31-AUG-1998; 98JP-0244755.  
XX  
PA (AGEN ) KOGYO GIJUTSUINCHO.  
XX  
DR WPI; 2000-075225/07.  
XX  
PT Nucleotide sequence of ribozyme useful as antiviral and gene expression  
suppression agents -  
XX  
XX Claim 1; Page 1; 24pp; Japanese.  
XX

KW CPP32; apoptosis; gene therapy; ss.  
 XX Synthetic.  
 OS  
 XX  
 PN EPI097993-A2.  
 XX  
 PD 09-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000EP-0250368.  
 XX  
 PR 05-NOV-1999; 99JP-0316133.  
 XX  
 XX (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.  
 PA (TAIR/) TAIRA K.  
 XX  
 XX TAIRA K, Warashina M, Kuwabara T, Kawasaki H;  
 PI WPI; 2001-357832/38.  
 XX  
 DR Novel chimeric molecule useful for clarifying biological function of  
 XX target nucleic acid and for treating viral diseases, and Alzheimer's  
 PT disease, comprises region with binding affinity for molecule capable of  
 PT sliding  
 XX  
 PS Example 1; Page 47; 76pp; English.  
 XX  
 CC The present sequence is that of novel ribozyme CPP Rz2, which is  
 CC targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related  
 CC gene encoding procaspase-3. CPP Rz2 was used to demonstrate the high  
 CC efficacy of hybrid ribozymes linked to a constitutive transport  
 CC element (CTE, See AAF30944) for inhibition gene expression.  
 CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see  
 CC AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme  
 CC expression plasmids and procaspase-3 expression levels were  
 CC determined by Western blotting after 36 hr. CTE-linked ribozymes  
 CC were more effective than their conventional counterparts for  
 CC inhibiting CPP32 gene expression. The CTE moiety facilitates  
 CC cleavage of RNA previously considered refractory because of local  
 CC high-order structure. It binds to RNA helicase A, which has  
 CC functions of binding to RNA, sliding and unwinding its high-order  
 CC structure. Chimeric molecules of the invention, including  
 CC CTE-ribozymes, and expression vectors, are used to prevent or  
 CC treat viral diseases, diseases associated with apoptosis or  
 CC diseases associated with abnormal gene expression (claimed). They  
 CC are also used in a claimed method of specifically cleaving a target  
 CC nucleic acid, especially a viral gene, protooncogene or a gene  
 CC associated with apoptosis.  
 XX  
 SQ Sequence 142 BP; 38 A; 36 C; 35 G; 33 U; 0 other;  
 Query Match 57.4%; Score 81; DB 22; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACCGUGGUUCCGUGAGUGGUUAUCACGUCUACACGCGAAAGGUCCCGG 60  
 DB 1 ACCGUGGUUCCGUGAGUGGUUAUCACGUCUACACGCGAAAGGUCCCGG 60  
 QY 61 UUCGAAACCGGGCACUACAAA 81  
 DB 61 UUCGAAACCGGGCACUACAAA 81  
 RESULT 15  
 AAF90394  
 ID AAF90394 standard; RNA; 142 BP.  
 XX  
 AC AAF90394;  
 XX  
 XX 06-AUG-2001 (first entry)  
 XX  
 DE Mouse procaspase-3 mRNA targeted ribozyme CPP Rz3.  
 XX

KW Ribozyme; constitutive transport element; mouse; procaspase-3;  
 KW CPP32; apoptosis; gene therapy; ss.  
 XX Synthetic.  
 OS  
 XX  
 PN EPI097993-A2.  
 XX  
 PD 09-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000EP-0250368.  
 XX  
 PR 05-NOV-1999; 99JP-0316133.  
 XX  
 XX (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.  
 PA (TAIR/) TAIRA K.  
 XX  
 XX TAIRA K, Warashina M, Kuwabara T, Kawasaki H;  
 PI WPI; 2001-357832/38.  
 XX  
 DR Novel chimeric molecule useful for clarifying biological function of  
 XX target nucleic acid and for treating viral diseases, and Alzheimer's  
 PT disease, comprises region with binding affinity for molecule capable of  
 PT sliding  
 XX  
 PS Example 1; Page 48; 76pp; English.  
 XX  
 CC The present sequence is that of novel ribozyme CPP Rz3, which is  
 CC targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related  
 CC gene encoding procaspase-3. CPP Rz3 was used to demonstrate the high  
 CC efficacy of hybrid ribozymes linked to a constitutive transport  
 CC element (CTE, See AAF30944) for inhibition gene expression.  
 CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see  
 CC AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme  
 CC expression plasmids and procaspase-3 expression levels were  
 CC determined by Western blotting after 36 hr. CTE-linked ribozymes  
 CC were more effective than their conventional counterparts for  
 CC inhibiting CPP32 gene expression. The CTE moiety facilitates  
 CC cleavage of RNA previously considered refractory because of local  
 CC high-order structure. It binds to RNA helicase A, which has  
 CC functions of binding to RNA, sliding and unwinding its high-order  
 CC structure. Chimeric molecules of the invention, including  
 CC CTE-ribozymes, and expression vectors, are used to prevent or  
 CC treat viral diseases, diseases associated with apoptosis or  
 CC diseases associated with abnormal gene expression (claimed). They  
 CC are also used in a claimed method of specifically cleaving a target  
 CC nucleic acid, especially a viral gene, protooncogene or a gene  
 CC associated with apoptosis.  
 XX  
 SQ Sequence 142 BP; 37 A; 40 C; 34 G; 31 U; 0 other;  
 Query Match 57.4%; Score 81; DB 22; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACCGUGGUUCCGUGAGUGGUUAUCACGUCUACACGCGAAAGGUCCCGG 60  
 DB 1 ACCGUGGUUCCGUGAGUGGUUAUCACGUCUACACGCGAAAGGUCCCGG 60  
 QY 61 UUCGAAACCGGGCACUACAAA 81  
 DB 61 UUCGAAACCGGGCACUACAAA 81  
 Search completed: September 13, 2003, 09:52:33  
 Job time : 205.848 secs

```

FT      stem_loop      /*tag= d
FT      56..72
FT      /*tag= e
FT      misc_binding
FT      73..78
FT      /*tag= f
FT      /bound_moiety= "trna-val_t-mzl"
FT      /note= "Forms a double-stranded region with nucleotides
FT      19-14 of itself"
FT      81..88
FT      /*tag= g
FT      /bound_moiety= "trna-val_t-mzl"
FT      /note= "Forms a double-stranded region with nucleotides
FT      11-4 of itself"
FT      95..107
FT      /*tag= h
FT      stem_loop
FT      111..128
FT      /*tag= i

```

XX JP2002119283-A.

XX PD 23-APR-2002.

XX PF 13-OCT-2000; 2000JP-0313320.

XX PR 13-OCT-2000; 2000JP-0313320.

XX PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.

XX DR WPI; 2002-483792/52.

XX A nucleic acid enzyme which has selective and effective eradicating  
 PT activity towards harmful cells by acquiring cleavage activity of a  
 PT specific target RNA by recognition of the other RNA molecule

XX PS Disclosure; Fig 7; 17pp; Japanese.

XX CC The invention relates to a nucleic acid enzyme with modifiable RNA  
 CC cleavage activity. More specifically the invention relates to a nucleic  
 CC acid enzyme, trans maxizyme, which has selective and effective  
 CC eradicating activity towards harmful cells by acquiring cleavage activity  
 CC of a specific target RNA by recognition of the other RNA molecule. The  
 CC enzyme of the invention is useful for cleaving target RNA and is useful  
 CC in treating diseases caused by the target RNA. This polynucleotide  
 CC sequence represents the trna-val t-mzl sequence related to the maxizyme  
 CC enzyme of the invention.

XX SQ Sequence 138 BP; 31 A; 38 C; 32 G; 37 U; 0 other;

```

Query Match      57.4%; Score 81; DB 24; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUUACACGCGAAAGGUCGCCGG 60
          |||||
Db       1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUUACACGCGAAAGGUCGCCGG 60
          |||||

```

QY 61 UUCGAAACCGGGCACUACAAA 81

Db 61 UUCGAAACCGGGCACUACAAA 81

RESULT 13

AAF90392

ID AAF90392 standard; RNA; 142 BP.

XX AC AAF90392;

XX DT 06-AUG-2001 (first entry)

XX DE Mouse procaspase-3 mRNA targeted ribozyme CPP Rz1.

XX DE Ribozyme; constitutive transport element; mouse; procaspase-3;

KW CPP32; apoptosis; gene therapy; ss.

```

XX OS Synthetic.
XX PN EPI097993-A2.
XX PD 09-MAY-2001.
XX PF 03-NOV-2000; 2000EP-0250368.
XX PR 05-NOV-1999; 99JP-0316133.
XX PA (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
XX PA (TAIR/) TAIRA K.
XX PI Taira K, Warashina M, Kuwabara T, Kawasaki H;
XX DR WPI; 2001-357832/38.
XX Novel chimeric molecule useful for clarifying biological function of
XX target nucleic acid and for treating viral diseases, and Alzheimer's
XX disease, comprises region with binding affinity for molecule capable of
XX sliding

```

Example 1; Page 47; 76pp; English.

XX CC The present sequence is that of novel ribozyme CPP Rz1, which is  
 CC targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related  
 CC gene encoding procaspase-3. CPP Rz1 was used to demonstrate the high  
 CC efficacy of hybrid ribozymes linked to a constitutive transport  
 CC element (CTE, See AAF30944) for inhibition gene expression.  
 CC 5 Ribozymes for different sites in CPP32 mRNA were designed (see  
 CC AAF90392-96). Mouse NIH3T3 cells were transfected with ribozyme  
 CC expression plasmids and procaspase-3 expression levels were  
 CC determined by Western blotting after 36 hr. CTE-linked ribozymes  
 CC were more effective than their conventional counterparts for  
 CC inhibiting CPP32 gene expression. The CTE moiety facilitates  
 CC cleavage of RNA previously considered refractory because of local  
 CC high-order structure. It binds to RNA helicase A, which has  
 CC functions of binding to RNA, sliding and unwinding its high-order  
 CC structure. Chimeric molecules of the invention, including  
 CC CTE-ribozymes, and expression vectors, are used to prevent or  
 CC treat viral diseases, diseases associated with apoptosis or  
 CC diseases associated with abnormal gene expression (claimed). They  
 CC are also used in a claimed method of specifically cleaving a target  
 CC nucleic acid, especially a viral gene, protooncogene or a gene  
 CC associated with apoptosis.

XX SQ Sequence 142 BP; 36 A; 42 C; 37 G; 27 U; 0 other;

```

Query Match      57.4%; Score 81; DB 22; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUUACACGCGAAAGGUCGCCGG 60
          |||||
Db       1 ACCGUGGUUCCGUGAGUGGUUACACGUCGCUUACACGCGAAAGGUCGCCGG 60
          |||||

```

QY 61 UUCGAAACCGGGCACUACAAA 81

Db 61 UUCGAAACCGGGCACUACAAA 81

RESULT 14

AAF90393

ID AAF90393 standard; RNA; 142 BP.

XX AC AAF90393;

XX DT 06-AUG-2001 (first entry)

XX DE Mouse procaspase-3 mRNA targeted ribozyme CPP Rz2.

XX DE Ribozyme; constitutive transport element; mouse; procaspase-3;

KW Ribozyme; constitutive transport element; mouse; procaspase-3;



CC sequence represents the tRNA-val promoter sequence relating to the  
 CC maxizyme enzyme of the invention.

SQ Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;

Query Match 57.4%; Score 81; DB 24; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;  
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGAGUGAGUGGUUAUCACGUCGCUAACACGCGGAAAGGUCGCCGG 60  
 |||||  
 Db 1 ACCGUGGUUCCGAGUGAGUGGUUAUCACGUCGCUAACACGCGGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGGCACUACAAA 81  
 |||||

Db 61 UUCGAAACCGGGCACUACAAA 81

# RESULT 9

ABX12785

ID ABX12785 standard; RNA; 88 BP.

XX

AC ABX12785;

XX

DT 15-MAY-2003 (first entry)

XX

XX

DE Human RNA sequence relating to novel maxizyme.

XX

KW Human; maxizyme; target mRNA; helicase activity; viral disease;

KW human immunodeficiency virus; HIV; hepatitis C; hepatitis B; cancer;

KW apoptosis-associated disease; Alzheimer's disease; Parkinson's disease;

KW autoimmune disease; inflammatory disease; genetic disorder;

KW mRNA cleavage; virucide; neurotropic; antiparkinsonian; cytostatic;

KW antiinflammatory; immunosuppressive; ss.

XX

OS Homo sapiens.

XX

PN WO200292821-A1.

XX

PD 21-NOV-2002.

XX

PF 30-APR-2002; 2002WO-JP04322.

XX

PR 01-MAY-2001; 2001JP-0134469.

XX

PA (NRAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX

PA (TAIS) TAISSHO PHARM CO LTD.

XX

PA (GENO-) GENOFUNCTION INC.

XX

PI Taira K, Warashina T, Warashina M, Kawasaki H, Hara T, Nozawa I;

XX

XX WPI; 2003-129298/12.

DR

XX

PT Maxizyme binding to a molecule with helicase activity for treatment of

XX

PT viral infection cancer and autoimmune disease

XX

PS Claim 11; Page 30-31; 36pp; Japanese.

XX

CC The present invention relates to a novel maxizyme that can bind to a

CC target mRNA molecule or a molecule having helicase activity. The

CC maxizyme is useful for the prevention and treatment of viral diseases

CC such as human immunodeficiency virus (HIV), hepatitis C or hepatitis B,

CC apoptosis-associated diseases such as Alzheimer's and Parkinson's

CC diseases, cancer, autoimmune diseases, inflammatory diseases and

CC genetic disorders. The maxizyme binds to and cleaves target mRNA

CC irrespective of the higher-order structure of the latter. The present

CC sequence represents a human RNA sequence relating to the present

XX invention.

SQ Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;

Query Match 57.4%; Score 81; DB 25; Length 88;

Best Local Similarity 100.0%; Pred. No. 1.9e-18;

Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGAGUGAGUGGUUAUCACGUCGCUAACACGCGGAAAGGUCGCCGG 60  
 |||||

Db 1 ACCGUGGUUCCGAGUGAGUGGUUAUCACGUCGCUAACACGCGGAAAGGUCGCCGG 60

QY 61 UUCGAAACCGGGCACUACAAA 81  
 |||||

Db 61 UUCGAAACCGGGCACUACAAA 81

# RESULT 10

ABZ21212

ID ABZ21212 standard; DNA; 117 BP.

XX

AC ABZ21212;

XX

DT 04-APR-2003 (first entry)

XX

DE tet 01-tRNAval sequence, SEQ ID 1.

XX

KW Antiviral; gene therapy; ribozyme expression cassette;

KW tetracyclin operator; promoter; ribozyme; anti-HIV; ds.

XX

OS Synthetic.

XX

PN JP2002262880-A.

XX

PD 17-SEP-2002.

XX

PF 09-MAR-2001; 2001JP-0067253.

XX

PR 09-MAR-2001; 2001JP-0067253.

XX

PA (KOKU-) KOKURITSU YOKO EISEI KENKYUSHO.

XX

PA (TAKE/) TAKEBE Y.

XX

PA (OKAW/) OKAWA J.

XX

XX WPI; 2003-132124/13.

DR

XX

XX

PT Ribozyme expression cassette, useful for preparing a cell insensitive

XX to HIV and for inhibiting growth of HIV, comprises a tetracyclin

XX operator, at least one promoter and a sequence encoding a ribozyme

XX successively from the upstream side

XX

PS Claim 6; Page 15; 27pp; Japanese.

XX

CC The present invention relates to a ribozyme expression cassette

XX comprising a tetracyclin operator, at least one promoter and a DNA

XX sequence encoding a ribozyme successively from the 5' end. The

XX tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from

XX the transcription initiating site of the promoter. The expression

XX cassette is useful in a method for preparing a cell having no sensitivity

XX to HIV, and for inhibiting the growth of HIV. To illustrate the

XX invention, a tet 01-human tRNAval promoter cassette was constructed,

XX using the present sequence.

XX

SQ Sequence 117 BP; 31 A; 28 C; 26 G; 32 T; 0 other;

Query Match 57.4%; Score 81; DB 25; Length 117;

Best Local Similarity 76.5%; Pred. No. 2e-18;

Matches 62; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGGUUCCGAGUGAGUGGUUAUCACGUCGCUAACACGCGGAAAGGUCGCCGG 60  
 |||||

Db 29 ACCGTTGGTTTCGTTAGTGTAGTGTATACGTTGCGCTTAACACGCGAAAGGTCGCCGG 88

QY 61 UUCGAAACCGGGCACUACAAA 81  
 :|||||

Db 89 TTCGAAACCGGGCACUACAAA 109

# RESULT 11



PT disease, comprises region with binding affinity for molecule capable of  
 PT sliding -  
 XX  
 PS Example 1; Page 48; 76pp; English.  
 XX  
 CC The present sequence is that of novel ribozyme CPP R23, which is  
 CC targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related  
 CC gene encoding procaspase-3. CPP R23 was used to demonstrate the high  
 CC efficacy of hybrid ribozymes linked to a constitutive transport  
 CC element (CTE). See AAF30944 for inhibition gene expression.  
 CC 5 ribozymes for different sites in CPP32 mRNA were designed (see  
 CC AA90392-96). Mouse NIH3T3 cells were transfected with ribozyme  
 CC expression plasmids and procaspase-3 expression levels were  
 CC determined by Western blotting after 36 hr. CTE-linked ribozymes  
 CC were more effective than their conventional counterparts for  
 CC inhibiting CPP32 gene expression. The CTE moiety facilitates  
 CC cleavage of RNA previously considered refractory because of local  
 CC high-order structure. It binds to RNA helicase A, which has  
 CC functions of binding to RNA, sliding and unwinding its high-order  
 CC structure. Chimeric molecules of the invention, including  
 CC CTE-ribozymes, and expression vectors, are used to prevent or  
 CC treat viral diseases, diseases associated with apoptosis or  
 CC diseases associated with abnormal gene expression (claimed). They  
 CC are also used in a claimed method of specifically cleaving a target  
 CC nucleic acid, especially a viral gene, protooncogene or a gene  
 CC associated with apoptosis.  
 XX  
 SQ Sequence 141 BP; 37 A; 37 C; 35 G; 32 U; 0 other;  
 Query Match 58.6%; Score 82.6; DB 22; Length 141;  
 Best Local Similarity 80.2%; Pred. No. 5.9e-19;  
 Matches 97; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
 QY 1 ACCGUGGUUCCGAGUGUGUAGUGUUAUACACGUGGCUAACACGCGAAAGGUCGCCGG 60  
 DB 1 ACCGUGGUUCCGAGUGUGUAGUGUUAUACACGUGGCUAACACGCGAAAGGUCGCCGG 60  
 QY 61 UUCGAAACCGGGACACACACACACACACACACACACACACACACACACACACACAC 120  
 DB 61 UUCGAAACCGGGACACACACACACACACACACACACACACACACACACACACACAC 120  
 QY 121 G 121  
 DB 121 G 121  
 RESULT 7  
 AA210600  
 ID AA210600 standard; RNA; 88 BP.  
 AC AA210600;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Nucleotide sequence of tRNA-val.  
 XX  
 KW Nucleic acid enzyme; maxizyme; allosteric RNA-cleaving activity;  
 KW RNA cleavage; chronic myeloid leukemia;  
 KW Philadelphia chromosome abnormality; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9946388-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 11-MAR-1999; 99WO-JP01187.  
 XX  
 PR 12-MAR-1998; 98JP-0060969.  
 PR 30-OCT-1998; 98JP-0311098.  
 XX  
 XX (TAIS) TAISHO PHARM CO LTD.  
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

XX  
 PI Taira K, Kuwabara T, Hitoshio A;  
 XX  
 DR WPI; 1999-551415/46.  
 XX  
 PT Nucleic acid enzyme having allosteric RNA-cleaving activity, used for  
 PT treatment of chronic myeloid leukemia -  
 XX  
 PS Claim 8; Page 55; 93pp; Japanese.  
 XX  
 CC The specification describes nucleotide sequences which make up the  
 CC left and right arms of a nucleic acid enzyme (maxizyme). The maxizyme  
 CC has allosteric RNA-cleaving activity on a specific target RNA. The  
 CC maxizyme can be used for efficient cleavage of RNA molecules at  
 CC specific points, especially for the prevention and treatment of  
 CC chronic myeloid leukemia and Philadelphia chromosome abnormality.  
 CC The present sequence is used in the course of the invention.  
 XX  
 SQ Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;  
 Query Match 57.4%; Score 81; DB 20; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;  
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACCGUGGUUCCGAGUGUGUAGUGUUAUACACGUGGCUAACACGCGAAAGGUCGCCGG 60  
 DB 1 ACCGUGGUUCCGAGUGUGUAGUGUUAUACACGUGGCUAACACGCGAAAGGUCGCCGG 60  
 QY 61 UUCGAAACCGGGACACACACACACACACACACACACACACACACACACACACACAC 81  
 DB 61 UUCGAAACCGGGACACACACACACACACACACACACACACACACACACACACACAC 81  
 RESULT 8  
 AAL40450  
 ID AAL40450 standard; tRNA; 88 BP.  
 XX  
 AC AAL40450;  
 XX  
 DT 19-SEP-2002 (first entry)  
 XX  
 DE Maxizyme related tRNA-val promoter sequence.  
 XX  
 KW Enzyme; modifiable RNA cleavage activity; maxizyme-constituting RNA;  
 KW trans maxizyme; tRNA-val; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2002119283-A.  
 XX  
 PD 23-APR-2002.  
 XX  
 PF 13-OCT-2000; 2000JP-0313320.  
 XX  
 PR 13-OCT-2000; 2000JP-0313320.  
 XX  
 PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.  
 XX  
 XX WPI; 2002-483792/52.  
 XX  
 PT A nucleic acid enzyme which has selective and effective eradicating  
 PT activity towards harmful cells by acquiring cleavage activity of a  
 PT specific target RNA by recognition of the other RNA molecule -  
 XX  
 PS Claim 12; Page 2; 17pp; Japanese.  
 XX  
 CC The invention relates to a nucleic acid enzyme with modifiable RNA  
 CC cleavage activity. More specifically the invention relates to a nucleic  
 CC acid enzyme, trans maxizyme, which has selective and effective  
 CC eradicating activity towards harmful cells by acquiring cleavage activity  
 CC of a specific target RNA by recognition of the other RNA molecule. The  
 CC enzyme of the invention is useful for cleaving target RNA and is useful  
 CC in treating diseases caused by the target RNA. This polynucleotide



CC The invention provides nucleotide sequences of hammerhead ribozymes  
 CC that can be used as antiviral and gene expression suppression agents.  
 CC The ribozymes have high stability in vivo. The present sequence  
 CC represents an example of such a ribozyme.

XX SQ Sequence 142 BP; 39 A; 38 C; 37 G; 28 U; 0 other;

Query Match 100.0%; Score 141; DB 21; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-39;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCG 60  
 DB 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCG 60  
 QY 61 UUCGAAACCGGGCACUACAAACACACACACACACACACACACACACACACACACACAC 120  
 DB 61 UUCGAAACCGGGCACUACAAACACACACACACACACACACACACACACACACACACAC 120  
 QY 121 GGGCAGUCGGAACGGUUU 141  
 DB 121 GGGCAGUCGGAACGGUUU 141

## RESULT 2

RAZ58590  
 ID AAZ58590 standard; RNA; 136 BP.

XX AC AAZ58590;

XX 31-MAR-2000 (first entry)

XX DE Nucleotide sequence of hammerhead ribozyme Rz2.

XX KW Hammerhead ribozyme; antiviral; gene expression; ss.

XX OS Synthetic.

XX PN JP2990268-B1.

XX PD 13-DEC-1999.

XX PF 31-AUG-1998; 98JP-0244755.

XX PR 31-AUG-1998; 98JP-0244755.

XX PA (AGEN) KOGYO GIJUNSUINCHO.

XX DR WPI; 2000-075225/07.

XX PT Nucleotide sequence of ribozyme useful as antiviral and gene expression  
 PT suppression agents.

XX PS Claim 1; Page 1; 24pp; Japanese.

XX CC The invention provides nucleotide sequences of hammerhead ribozymes  
 CC that can be used as antiviral and gene expression suppression agents.  
 CC The ribozymes have high stability in vivo. The present sequence  
 CC represents an example of such a ribozyme.

XX SQ Sequence 136 BP; 36 A; 35 C; 37 G; 28 U; 0 other;

Query Match 84.4%; Score 119; DB 21; Length 136;  
 Best Local Similarity 95.7%; Pred. No. 1.3e-31;  
 Matches 135; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCG 60  
 DB 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCG 60  
 QY 61 UUCGAAACCGGGCACUACAAACACACACACACACACACACACACACACACACACACAC 120  
 DB 61 UUCGAAACCGGGCACUACAA-----ACACACACACACACACACACACACACACAC 114

QY 121 GGGCAGUCGGAACGGUUU 141  
 DB 115 GGGCAGUCGGAACGGUUU 135

## RESULT 3

ABZ21217  
 ID ABZ21217 standard; DNA; 175 BP.

XX AC ABZ21217;

XX 04-APR-2003 (first entry)

XX DE Nucleotide sequence of ribozyme expressing cassette, SEQ ID 6.

XX KW Antiviral; gene therapy; ribozyme expression cassette;  
 KW tetracyclin operator; promoter; ribozyme; anti-HIV; ds.

XX OS Synthetic.

XX PN JP2002262880-A.

XX PD 17-SEP-2002.

XX PF 09-MAR-2001; 2001JP-0067253.

XX PR 09-MAR-2001; 2001JP-0067253.

XX PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.

XX PA (TAKE/) TAKEBE Y.

XX PA (OKAW/) OKAWA J.

XX WPI; 2003-132124/13.

XX DR Ribozyme expression cassette, useful for preparing a cell insensitive  
 XX to HIV and for inhibiting growth of HIV, comprises a tetracyclin  
 XX operator, at least one promoter and a sequence encoding a ribozyme  
 XX successively from the upstream side -

XX PS Disclosure; Page 16; 27pp; Japanese.

XX CC The present invention relates to a ribozyme expression cassette  
 XX comprising a tetracyclin operator, at least one promoter and a DNA  
 XX sequence encoding a ribozyme successively from the 5' end. The  
 XX tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from  
 XX the transcription initiating site of the promoter. The expression  
 XX cassette is useful in a method for preparing a cell having no sensitivity  
 XX to HIV, and for inhibiting the growth of HIV. The present sequence was  
 XX used to illustrate the invention.

XX SQ Sequence 175 BP; 48 A; 40 C; 41 G; 46 T; 0 other;

Query Match 67.5%; Score 95.2; DB 25; Length 175;  
 Best Local Similarity 69.9%; Pred. No. 2.6e-23;  
 Matches 102; Conservative 26; Mismatches 13; Indels 5; Gaps 2;

QY 1 ACCGUGGUGUCCGAGUGAGUGGUUAUCACGUGCCUUAACACGCGAAAGGUCGCCCG 60  
 DB 29 ACCGTTGGTTCCGTTAGTCTACTGCTTATCGCTTACACGCGAAGGTCGCCCG 88  
 QY 61 UUCGAAACCGGGCACUACAAA-----CCACACACACACACACACACACACACACAC 116  
 DB 89 TTCGAAACCGGGCACACTACAAAACCAACCAACGATAGATGCTGATGAGGACCGAAGGTC 148  
 QY 117 AAAC-GGGCAGUCGGAACGGUUU 141  
 DB 149 AAACITGACACTCCGGAAACGGTTTT 174

## RESULT 4

ABZ21216  
 ID ABZ21216 standard; DNA; 175 BP.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 08:06:21 ; Search time 204.348 seconds  
(without alignments)  
1862.612 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accguuguuucguagugu.....ggcacucggaacgguuuu 141

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	141	100.0	142	21	AAZ58591 Nucleotide sequenc
2	119	84.4	136	21	AAZ58590 Nucleotide sequenc
3	95.2	67.5	175	25	ABZ21217 Nucleotide sequenc
4	91.8	65.1	175	25	ABZ21216 Nucleotide sequenc
5	83.2	59.0	100	22	AAH47825 Human tRNA promote
6	82.6	58.6	141	22	AAF90395 Mouse procaspase-3
7	81	57.4	88	24	AAZ10600 Nucleotide sequenc
8	81	57.4	88	24	AAZ10450 Maxizyme related t

9	81	57.4	88	25	ABX12785 Human RNA sequence
10	81	57.4	117	25	ABZ21212 tet 01-TRNAVal seq
11	81	57.4	137	24	ABK51149 tRNA-Luc GUA Rz R1
12	81	57.4	138	24	AAZ10467 Maxizyme related t
13	81	57.4	142	22	AAF90392 Mouse procaspase-3
14	81	57.4	142	22	AAF90393 Mouse procaspase-3
15	81	57.4	142	22	AAF90394 Mouse procaspase-3
16	81	57.4	142	22	AAF90396 Mouse procaspase-3
17	81	57.4	151	22	AAF90357 DNA cassette for t
18	81	57.4	320	22	AAF90358 tRNAVal-linked rib
19	75	53.2	128	21	AAZ58592 Nucleotide sequenc
20	73.4	52.1	149	21	AAZ58594 Nucleotide sequenc
21	73	51.8	95	21	AAZ58593 Human placental tr
22	73	51.8	95	22	AAF90356 Plasmid pTV1. Syn
23	73	51.8	269	17	AAZ09848 Plasmid pBTv1-434
24	73	51.8	325	17	AAZ09849 Plasmid pBTv1-434
25	73	51.8	332	17	AAZ09852 Plasmid pZIP VI-43
26	73	51.8	406	17	AAZ09850 Plasmid pZIP VI-43
27	73	51.8	406	17	AAZ09851 Human cDNA differe
28	73	51.8	139904	24	ABK83562 Pol III transcript
29	69.8	49.5	132	18	AAZ92275 Pol III transcript
30	69.8	49.5	132	19	AAZ57890 Cassette pMT. Sy
31	69.8	49.5	132	22	AAZ60208 Sequence of a lowe
32	69.4	49.2	109	21	AAZ58601 Sequence of a sens
33	66.8	47.4	113	21	AAZ58596 Nucleic acid seque
34	66	46.8	110	21	AAZ58595 Sequence of a lowe
35	65	46.1	106	21	AAZ58602 Drosophila melanog
36	63.8	45.2	43226	20	AAZ60263 Drosophila melanog
37	53.6	38.0	4669	23	ABL02136 Drosophila melanog
38	53.2	37.7	2289	23	ABL04712 Drosophila melanog
39	53.2	37.7	2451	23	ABL24834 Drosophila melanog
40	53.2	37.7	3886	23	ABL24836 Drosophila melanog
41	53.2	37.7	22967	23	ABL12942 Drosophila melanog
42	50	35.5	7799	23	ABL30068 Drosophila melanog
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44	50	35.5	27433	23	ABL20312 Drosophila melanog
45	46.8	33.2	121	25	ABZ21226 PCR primer CCR5-Rz

## ALIGNMENTS

RESULT 1  
AAZ58591  
ID AAZ58591 standard; RNA; 142 BP.  
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AC AAZ58591;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Nucleotide sequence of hammerhead ribozyme Rz3.  
XX  
KW Hammerhead ribozyme; antiviral; gene expression; ss.  
XX  
OS Synthetic.  
XX  
PN JP2990268-B1.  
XX  
PD 13-DEC-1999.  
XX  
PF 31-AUG-1998; 98JP-0244755.  
XX  
PR 31-AUG-1998; 98JP-0244755.  
XX  
PA (AGEN ) KOGYO GIJUTSUINCHO.  
XX  
DR WPI; 2000-075225/07.  
XX  
PT Nucleotide sequence of ribozyme useful as antiviral and gene expression  
XX  
PS suppression agents -  
XX  
PS Claim 1; Page 1; 24pp; Japanese.  
XX

BASE COUNT 23 a 25 c 21 g 19 t  
ORIGIN

Query Match 57.4%; Score 81; DB 6; Length 88;  
Best Local Similarity 76.5%; Pred. No. 8.3e-13;  
Matches 62; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

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Job time : 1436.54 secs

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Best Local Similarity 75.3%; Pred. No. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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RESULT 13
AB080624
LOCUS      153 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
anti-mSryRNA/Rz6.
ACCESSION AB080624
VERSION AB080624.1 GI:22531657
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE 1
AUTHORS    Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
Nishino,K., Nakayama,A. and Taira,K.
TITLE      Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL    Unpublished
REFERENCE 2 (bases 1 to 153)
AUTHORS    Tachi,C.
TITLE      Direct Submission
JOURNAL    Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
Veterinary Medicine, Lab. Developmental and Reproductive
Biotechnology; 1-17-71, Fuchinobe, Sagamihara-shi 229-8501, Japan
(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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RESULT 14
AX453846
LOCUS      88 bp      mRNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 5 from Patent EP1213351.

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ACCESSION AX453846
VERSION AX453846.1 GI:21713515
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE 1
AUTHORS    Taira,K., Warashina,M. and Warashina,T.
TITLE      Nucleic acid enzymes acquiring an activity for cleaving a target
            rna by recognising another molecule
JOURNAL    Patent: EP 1213351-A 5 12-JUN-2002;
            National Institute of Advanced Industrial Science and Technology
            (JP)
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Matches 62; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

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QY 61 UUCGAAACCGGGCACUACAA 81
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Db 61 TTCGAACCGGGCACTACAA 81

RESULT 15
BD143502
LOCUS      88 bp      RNA      linear      PAT 17-JAN-2003
DEFINITION Nucleic acid enzyme acquiring activity of cleaving other specific
            target RNA by recognizing RNA molecule.
ACCESSION BD143502
VERSION BD143502.1 GI:27849260
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE 1 (bases 1 to 88)
AUTHORS    Taira,K., Warashina,M. and Warashina,T.
TITLE      Nucleic acid enzyme acquiring activity of cleaving other specific
            target RNA by recognizing RNA molecule
JOURNAL    Patent: JP 2002119283-A 5 23-APR-2002;
            DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
            SCIENCE AND P T BAKRIE AND BROTHERS,JAPAN BIO INDUSTRY ASSOCIATION,
            TECHNOLOGY
            OS Artificial Sequence
            PN JP 2002119283-A/5
            PD 23-APR-2002
            PF 13-OCT-2000 JP 2000313320
            PI KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO WARASHINA PC
            C12N15/09,A61K38/46,A61K38/46,A61K48/00,A61P31/12,A61P35/00, PC
            C12N1/25,
            PC C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/25,C12Q1/68,C12N15/
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RESULT 10
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DEFINITION
ACCESSION AB080621
VERSION   AB080621.1 GI:22531654
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
          artificial sequences.
REFERENCE
AUTHORS   Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
          Nishino,K., Nakayama,A. and Taira,K.
TITLE     Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL   Unpublished
AUTHORS   Tachi,C.
JOURNAL   Direct Submission
          Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
          Veterinary Medicine, Lab. Developmental and Reproductive
          Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
          (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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QY      61  UUCGAAACCGGGACUACAAACCAA 85
       :|||||:|||||:||||| 11
Db      61  TTCGAAACCGGGCACTACAAAACCA 85

RESULT 11
LOCUS   AB080622 Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
DEFINITION
ACCESSION AB080622
VERSION   AB080622.1 GI:22531655
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
          artificial sequences.
REFERENCE
AUTHORS   Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
          Nishino,K., Nakayama,A. and Taira,K.
TITLE     Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL   Unpublished
AUTHORS   Tachi,C.
JOURNAL   Direct Submission
          Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
          Veterinary Medicine, Lab. Developmental and Reproductive
          Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
          (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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Best Local Similarity 75.3%; Pred. NO. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

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Db      61  TTCGAAACCGGGCACTACAAAACCA 85

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TITLE     Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL   Unpublished
AUTHORS   Tachi,C.
TITLE     Direct Submission
JOURNAL   Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
          Veterinary Medicine, Lab. Developmental and Reproductive
          Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
          (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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Query Match      58.0%; Score 81.8; DB 12; Length 153;
Best Local Similarity 75.3%; Pred. NO. 4.6e-13;
Matches 64; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

QY      1  ACCGUGGUUCCGAGUGUAGUACGUCUACGCGUACACGCGAAGGUCGCCCGG 60
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QY      61  UUCGAAACCGGGACUACAAACCAA 85
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Db      61  TTCGAAACCGGGCACTACAAAACCA 85

RESULT 12
LOCUS   AB080623 Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
DEFINITION
ACCESSION AB080623
VERSION   AB080623.1 GI:22531656
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
          artificial sequences.
REFERENCE
AUTHORS   Tachi,C., Nakamura,K., Horii,T., Murata,C., Nishimura,S.,
          Nishino,K., Nakayama,A. and Taira,K.
TITLE     Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
JOURNAL   Unpublished
AUTHORS   Tachi,C.
JOURNAL   Direct Submission
          Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
          Veterinary Medicine, Lab. Developmental and Reproductive
          Biotechnology; 1-17-71, Fuchinobe, Sagami-hara-shi 229-8501, Japan
          (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
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Matches	68;	Conservative	20;	Mismatches 8; Indels 0; Gaps 0;
Qy	1	ACCGUUGGUUCCGUGAGUGUAGUGUUAUACGUGGCCUUAACACGCGAAAGGUCGCCGG	60	
Db	1	ACCGTGTGTTCCGTTAGTGTAGTGGTTATACGCTTCGCTTAACACGCGAAAGGTCGCCGG	60	
Qy	61	UUCGAAACCGGGCAGUACAAACCAACACACACACACU	96	
Db	61	TTCGAAACCGGGCAGTACAAAACCAACAAAAAAT	96	
RESULT 6				
AX138491			141 bp	mRNA linear PAT 30-MAY-2001
LOCUS				
DEFINITION			Sequence 52 from Patent EP1097993.	
ACCESSION			AX138491	
VERSION			AX138491.1	GI:14274387
KEYWORDS				
SOURCE			synthetic construct	
ORGANISM			synthetic construct	
REFERENCE			1	
AUTHORS			Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.	
TITLE			Functional ribozyme chimeric molecules capable of sliding	
JOURNAL			Patent: EP 1097993-A 52 09-MAY-2001.	
			Secretary of Agency of Industrial Science and Technology (JP) ;	
			Taira, Kazunari (JP)	
FEATURES			Location/Qualifiers	
source			1..141	
			/organism="synthetic construct"	
			/mol_type="mRNA"	
			/db_xref="taxon:32630"	
			/note="the nucleotide sequence of CPP Rz4"	
BASE COUNT	37 a	37 c	35 g	32 t
ORIGIN				
Query Match			58.6%;	Score 82.6; DB 6; Length 141;
Best Local Similarity			63.6%;	Pred. No. 2.7e-13;
Matches	77;	Conservative	20;	Mismatches 24; Indels 0; Gaps 0;
Qy	1	ACCGUUGGUUCCGUGAGUGUAGUGUUAUACGUGGCCUUAACACGCGAAAGGUCGCCGG	60	
Db	1	ACCGTGTGTTCCGTTAGTGTAGTGGTTATACGCTTCGCTTAACACGCGAAAGGTCGCCGG	60	
Qy	61	UUCGAAACCGGGCAGUACAAACCAACACACACACU	120	
Db	61	TTCGAAACCGGGCAGTACAAAACCAACTTCTAGATTTCGATGATGAGGCGCGAAG	120	
Qy	121 g	121		
Db	121 g	121		
RESULT 7				
BD015659			141 bp	RNA linear PAT 27-AUG-2002
LOCUS				
DEFINITION			Slidable functional chimeric molecule.	
ACCESSION			BD015659	
VERSION			BD015659.1	GI:22556796
KEYWORDS			JP 2001190282-A/52.	
SOURCE			synthetic construct	
ORGANISM			synthetic construct	

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COMMENT      OS      Artificial Sequence
PN      JP 2000069972-A/2
PD      07-MAR-2000
PF      31-AUG-1998 JP 1998244755
PI      KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI
PC      C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
FH      Key      Location/Qualifiers
FT      source      1..142
           Location/Qualifiers
FEATURES
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           /mol_type="genomic RNA"
           /db_xref="taxon:32630"
BASE COUNT    39 a 38 c 37 g 28 t
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Query Match      100.0%; Score 141; DB 6; Length 142;
Best Local Similarity 80.9%; Pred. No. 3.6e-30;
Matches 114; Conservative 27; Mismatches 0; Indels 0; Gaps 0;
QY      1 ACCGUGGUUCCGUGAGUGGUAUCACGUGCCUACACGCGGAAAGGUCCCGG 60
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 ACCGTTGGTTCCGTTAGTGTATCAGTTTCGCTAACACGCGGAAAGTCCCGG 60
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QY      61 UUCGAAACCGGGCACUACAAACACACACACACUGAGGAGGACCGGAAAGGUCCGAAAC 120
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 TTCGAAACCGGGCAGCTACAA-----ACACAACACTGATGAGGACCGGAAAGTCCGAAAC 114
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QY      121 GGGCAGCUGCGGAAACGGUUUU 141
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Db      115 GGGCACGTCGGAACGGTTTT 135
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FEATURES
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BASE COUNT    39 a 38 c 37 g 28 t
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Query Match      100.0%; Score 141; DB 6; Length 142;
Best Local Similarity 80.9%; Pred. No. 3.6e-30;
Matches 114; Conservative 27; Mismatches 0; Indels 0; Gaps 0;
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       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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QY      121 GGGCAGCUGCGGAAACGGUUUU 141
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Db      121 GGGCACGTCGGAACGGTTTT 141
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RESULT 2
E33203      E33203      136 bp      RNA      linear      PAT 31-JAN-2002
LOCUS      Expression system for functional nucleic acid transcription.
DEFINITION      E33203
ACCESSION      E33203
VERSION      E33203.1 GI:18623997
KEYWORDS      JP 2000069972-A/1.
SOURCE      synthetic construct
ORGANISM      synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 136)
AUTHORS      Tabira,K., Okawa,A. and OzeKI,S.
TITLE      Expression system for functional nucleic acid transcription
JOURNAL      Patent: JP 2000069972-A 1 07-MAR-2000;
               AGENCY OF IND SCIENCE & TECHNOL
COMMENT      OS      Artificial Sequence
PN      JP 2000069972-A/1
PD      07-MAR-2000
PF      31-AUG-1998 JP 1998244755
PI      KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI
PC      C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
FH      Key      Location/Qualifiers
FT      source      1..136
           Location/Qualifiers
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BASE COUNT    36 a 35 c 37 g 28 t
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Best Local Similarity 76.6%; Pred. No. 8.2e-24;
Matches 108; Conservative 27; Mismatches 0; Indels 6; Gaps 1;
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Db      1 ACCGTTGGTTCCGTTAGTGTATCAGTTTCGCTAACACGCGGAAAGTCCCGG 60
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QY      61 UUCGAAACCGGGCACUACAAACACACACACUGAGGAGGACCGGAAAGGUCCGAAAC 120
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 TTCGAAACCGGGCAGCTACAA-----ACACAACACTGATGAGGACCGGAAAGTCCGAAAC 114
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QY      121 GGGCAGCUGCGGAAACGGUUUU 141
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      115 GGGCACGTCGGAACGGTTTT 135
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RESULT 3
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LOCUS      Ribozyme expression system.
DEFINITION      BD174680
ACCESSION      BD174680
VERSION      BD174680.1 GI:29120370
KEYWORDS      JP 2002262880-A/5.
SOURCE      synthetic construct
ORGANISM      synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 175)
AUTHORS      Takebe,Y. and Okawa,J.
TITLE      Ribozyme expression system
JOURNAL      Patent: JP 2002262880-A 6 17-SEP-2002;
               DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
               YUTAKA TAKEBE,JUN OKAWA
COMMENT      OS      Artificial Sequence
PN      JP 2002262880-A/6
PD      17-SEP-2002
PF      09-MAR-2001 JP 2001067253
PI      YUTAKA TAKEBE,JUN OKAWA
PC      C12N15/09,A61K31/71,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
               C12N9/00.
PC      C12N15/00,C12N5/00
CC      Description of Artificial Sequence: the
               nucleotide sequence of
               ribozyme
CC      expressing cassette of the invention
FH      Key      Location/Qualifiers
FT      source      1..175
           Location/Qualifiers
FEATURES
   source      1..175
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
BASE COUNT    48 a 40 c 41 g 46 t
ORIGIN
Query Match      67.5%; Score 95.2; DB 6; Length 175;
Best Local Similarity 69.9%; Pred. No. 6.1e-17;
Matches 102; Conservative 26; Mismatches 13; Indels 5; Gaps 2;
QY      1 ACCGUGGUUCCGUGAGUGGUAUCACGUGCCUACACGCGGAAAGGUCCCGG 60
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      29 ACCGTTGGTTCCGTTAGTGTATCAGTTTCGCTAACACGCGGAAAGTCCCGG 88
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      61 UUCGAAACCGGGCACUACAA-----CCACACACACACUGAGGAGGACCGGAAAGGUCCG 116
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Db      89 TTCGAAACCGGGCAGCTACAAACACACACGATAGTCTGATGAGGACCGGAAAGTCCG 148
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QY      117 AAAC-GGGCAGCUGCGGAAACGGUUUU 141
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      149 AAACCTGACACTCCGGAACCGTTTT 174
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RESULT 4
BD174679
LOCUS      Ribozyme expression system.
DEFINITION      BD174679
ACCESSION      BD174679
VERSION      BD174679
KEYWORDS      JP 2002262880-A/5.
SOURCE      synthetic construct
ORGANISM      synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 175)
AUTHORS      Takebe,Y. and Okawa,J.
TITLE      Ribozyme expression system
JOURNAL      Patent: JP 2002262880-A 6 17-SEP-2002;
               DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
               YUTAKA TAKEBE,JUN OKAWA
COMMENT      OS      Artificial Sequence
PN      JP 2002262880-A/6
PD      17-SEP-2002
PF      09-MAR-2001 JP 2001067253
PI      YUTAKA TAKEBE,JUN OKAWA
PC      C12N15/09,A61K31/71,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
               C12N9/00.
PC      C12N15/00,C12N5/00
CC      Description of Artificial Sequence: the
               nucleotide sequence of
               ribozyme
CC      expressing cassette of the invention
FH      Key      Location/Qualifiers
FT      source      1..175
           Location/Qualifiers
FEATURES
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           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
BASE COUNT    48 a 40 c 41 g 46 t
ORIGIN
Query Match      67.5%; Score 95.2; DB 6; Length 175;
Best Local Similarity 69.9%; Pred. No. 6.1e-17;
Matches 102; Conservative 26; Mismatches 13; Indels 5; Gaps 2;
QY      1 ACCGUGGUUCCGUGAGUGGUAUCACGUGCCUACACGCGGAAAGGUCCCGG 60
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Db      29 ACCGTTGGTTCCGTTAGTGTATCAGTTTCGCTAACACGCGGAAAGTCCCGG 88
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QY      61 UUCGAAACCGGGCACUACAA-----CCACACACACACUGAGGAGGACCGGAAAGGUCCG 116
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      89 TTCGAAACCGGGCAGCTACAAACACACGATAGTCTGATGAGGACCGGAAAGTCCG 148
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QY      117 AAAC-GGGCAGCUGCGGAAACGGUUUU 141
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      149 AAACCTGACACTCCGGAACCGTTTT 174
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
BD174679
LOCUS      Ribozyme expression system.
DEFINITION      BD174679
ACCESSION      BD174679
VERSION      BD174679
KEYWORDS      JP 2002262880-A/5.
SOURCE      synthetic construct
ORGANISM      synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 175)
AUTHORS      Takebe,Y. and Okawa,J.
TITLE      Ribozyme expression system
JOURNAL      Patent: JP 2002262880-A 6 17-SEP-2002;
               DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
               YUTAKA TAKEBE,JUN OKAWA
COMMENT      OS      Artificial Sequence
PN      JP 2002262880-A/6
PD      17-SEP-2002
PF      09-MAR-2001 JP 2001067253
PI      YUTAKA TAKEBE,JUN OKAWA
PC      C12N15/09,A61K31/71,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
               C12N9/00.
PC      C12N15/00,C12N5/00
CC      Description of Artificial Sequence: the
               nucleotide sequence of
               ribozyme
CC      expressing cassette of the invention
FH      Key      Location/Qualifiers
FT      source      1..175
           Location/Qualifiers
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           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
BASE COUNT    48 a 40 c 41 g 46 t
ORIGIN
Query Match      67.5%; Score 95.2; DB 6; Length 175;
Best Local Similarity 69.9%; Pred. No. 6.1e-17;
Matches 102; Conservative 26; Mismatches 13; Indels 5; Gaps 2;
QY      1 ACCGUGGUUCCGUGAGUGGUAUCACGUGCCUACACGCGGAAAGGUCCCGG 60
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      29 ACCGTTGGTTCCGTTAGTGTATCAGTTTCGCTAACACGCGGAAAGTCCCGG 88
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QY      61 UUCGAAACCGGGCACUACAA-----CCACACACACACUGAGGAGGACCGGAAAGGUCCG 116
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      89 TTCGAAACCGGGCAGCTACAAACACACGATAGTCTGATGAGGACCGGAAAGTCCG 148
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QY      117 AAAC-GGGCAGCUGCGGAAACGGUUUU 141
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      149 AAACCTGACACTCCGGAACCGTTTT 174
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: September 13, 2003, 09:38:16 : Search time 1435.54 Seconds  
(without alignments)  
4018.170 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accgucguuuccgagugu.....ggcacgucggaacgguuu 141

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

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14: gb.vi.\*

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23: em.pat.\*

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25: em.pl.\*

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27: em.sts.\*

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29: em.vi.\*

30: em.htg.hum.\*

31: em.htg.inv.\*

32: em.htg.other.\*

33: em.htg.mus.\*

34: em.htg.pln.\*

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36: em.htg.mam.\*

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40: em.htgo.mus.\*

41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	141	100.0	142	6	E33204	E33204 Expression
2	119	84.4	136	6	E33203	E33203 Expression
3	95.2	67.5	175	6	BD174680	BD174680 Ribozyme
4	91.8	65.1	175	6	BD174679	BD174679 Ribozyme
5	83.2	59.0	100	6	E47174	E47174 Method for
6	82.6	58.6	141	6	AX138491	AX138491 Sequence
7	82.6	58.6	141	6	BD015659	BD015659 Slidable
8	81.8	58.0	153	12	AB080619	AB080619 Synthetic
9	81.8	58.0	153	12	AB080620	AB080620 Synthetic
10	81.8	58.0	153	12	AB080621	AB080621 Synthetic
11	81.8	58.0	153	12	AB080622	AB080622 Synthetic
12	81.8	58.0	153	12	AB080623	AB080623 Synthetic
13	81.8	58.0	153	12	AB080624	AB080624 Synthetic
14	81	57.4	88	6	AX453846	AX453846 Sequence
15	81	57.4	88	6	BD143502	BD143502 Nucleic a
16	81	57.4	88	6	BD182356	BD182356 Novel max
17	81	57.4	117	6	BD174675	BD174675 Ribozyme
18	81	57.4	137	6	AX429079	AX429079 Sequence
19	81	57.4	137	6	BD143601	BD143601 Method of
20	81	57.4	138	6	AX453858	AX453858 Sequence
21	81	57.4	142	6	AX138488	AX138488 Sequence
22	81	57.4	142	6	AX138489	AX138489 Sequence
23	81	57.4	142	6	AX138490	AX138490 Sequence
24	81	57.4	142	6	AX138492	AX138492 Sequence
25	81	57.4	142	6	BD015656	BD015656 Slidable
26	81	57.4	142	6	BD015657	BD015657 Slidable
27	81	57.4	142	6	BD015658	BD015658 Slidable
28	81	57.4	142	6	BD015660	BD015660 Slidable
29	81	57.4	151	6	AX138449	AX138449 Sequence
30	81	57.4	151	6	BD015617	BD015617 Slidable
31	81	57.4	320	6	AX138450	AX138450 Sequence
32	81	57.4	320	6	BD015618	BD015618 Slidable
33	75	53.2	128	6	E33205	E33205 Expression
34	73-4	52.1	149	6	E33207	E33207 Expression
35	73	51.8	95	6	AX138447	AX138447 Sequence
36	73	51.8	95	6	BD015615	BD015615 Slidable
37	73	51.8	95	6	E33206	E33206 Expression
38	73	51.8	183	11	G31283	G31283 sy905g1-L H
39	73	51.8	1396	9	HUMHTV1A	M15782 Human Htv1
40	73	51.8	139904	9	HS97D16	AL009179 Human DNA
41	69.8	49.5	132	6	AR041184	AR041184 Sequence
42	69.8	49.5	132	6	AR113038	AR113038 Sequence
43	69.8	49.5	132	6	I66463	I66463 Sequence 17
44	69.8	49.5	265074	2	AC103024	AC103024 Rattus no
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# ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
Accession  
E33204  
VERSION  
E33204.1 GI:18623998  
KEYWORDS  
JP 2000069972-A/2.  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.  
REFERENCE  
1 (bases 1 to 142)  
Tabira,K., Okawa,A. and Ozeki,S.  
AUTHORS  
Expression system for functional nucleic acid transcription  
TITLE  
Patent: JP 2000069972-A 2 07-MAR-2000;  
JOURNAL  
AGENCY OF IND SCIENCE & TECHNOL

E33204  
Expression system for functional nucleic acid transcription.  
142 bp RNA linear PAT 31-JAN-2002

Db 91 GGTTTCTATGGTGTAGTGTACACACGCTGGCCCTACACATGGAAGTCTCTATTGAA 150

Qy 67 AC 68

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Db 151 AC 152

Search completed: September 13, 2003, 09:43:48  
Job time : 164.75 secs



US-10-027-632-150960

[illegible]

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RESULT 9
US-10-027-632-135532/c
; Sequence 135532, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135532
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-135532

```

Query Match	35.9%	Score 50.6;	DB 13;	Length 603;
Best Local Similarity	61.5%;	Pred. No. 3.3e-08;		
Matches	40;	Conservative 16;	Mismatches 9;	Indels 0; Gaps 0;
QY	8	GUUUCGUGAGUGUGGUAUACGAGUUCGCCUUAACACGCGAAAGUCCCGGGUUCGAAA	67	
Db	136	: : : : :     : : : : :   :                 : : :		
		TGTAGTATGGTGTATCAAGTTAGCTTAGCTTACACACGTGAAGGTCCTCGTTTCGAAA	77	
QY	68	CCGGG	72	
Db	76	CCAGG	72	

```

RESULT 10
US-10-027-632-135520
; Sequence 135520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676

```

```
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 135520
/ LENGTH: 817
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-135520

Query Match          35.5%; Score 50; DB 13; Length 817;
Best Local Similarity 58.8%; Pred. No. 5.8e+08;
Matches 40; Conservative 17; Mismatches 11; Indels 0; Gaps 0

QY      6 UGUUUUCCGAGUGAUGUGGUAUCACGGCUCUAAACACGCAGAAGGCCCGGUGCA 65
       :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     304 TGGCTTCGTATCATGTGTTTATCATTCGCTCACACATGAAGGTACCATTGA 363

QY      66 AACCGGGC 73
       |||||||
Db     364 GACCGGGC 371
```

```

RESULT 11
US-10-027-632-148440/c
; Sequence 148440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148440
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-148440

```

Query Match	34.3%	Score 48.4	DB 13	Length 871
Best Local Similarity	59.3%	Pred. No. 2.2e-07		
Matches 44	Conservative 14	Mismatches 16	Indels 0	Gaps 0
QY	8	GUUCCGAGUGUGAGUGUUAUACAGUUCGCCUAACACGCGAAAGGUCGCCGUGUCGAA	67	
		: : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :		
Db	823	GGTCCGTAAGTGTAGTGGTATCATGTTCCGCTCACACGCGAAAGGTCCGGTTCGAAAC	764	
QY	68	CCGGSCACUACAAA	81	

```

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13960
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13960

Query Match
Best Local Similarity 46.7%; Score 65.8; DB 13; Length 704;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGUUGGUUCCGAGUGGUAUACACGUCGUAACACGCGAAAGGCCCGGUU 62
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::
Db 301 YGCAGGTTCCGTAGTGTAGTTCATCAGTTCGCTTCACACGCGAAAGGCCCGGTT 242
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::
QY 63 CGAAACCGGCG 73
    |||||
Db 241 CGAAACCGGCG 231
    |||||

```

```

RESULT 6
US-10-027-632-13961/c
; Sequence 13961, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13961
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13961

Query Match
Best Local Similarity 46.7%; Score 65.8; DB 13; Length 704;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 3 CGUUGGUUCCGAGUGGUAUACACGUCGUAACACGCGAAAGGCCCGGUU 62
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::
Db 301 YGCAGGTTCCGTAGTGTAGTTCATCAGTTCGCTTCACACGCGAAAGGCCCGGTT 242
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::
QY 63 CGAAACCGGCG 73
    |||||
Db 241 CGAAACCGGCG 231
    |||||

```

```

RESULT 7
US-10-027-632-150959

```

```

; Sequence 150959, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150959
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-150959

```

```

Query Match
Best Local Similarity 43.4%; Score 61.2; DB 13; Length 818;
Matches 46; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 6 UGCUUCCGAGUGGUAUACACGUCGUAACACGCGAAAGGCCCGGUUCCA 65
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::
Db 239 TGGTTCCGTAGTGTAGTTCATCAGTTCGCTTCACACGCGAAAGGCCCGGTTCCA 298
    : ||::||::||::||::||::||::||::||::||::||::||::||::||::
QY 66 AACCGG 71
    |||
Db 299 AACTGG 304
    |||

```

```

RESULT 8
US-10-027-632-150960
; Sequence 150960, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150960
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Human

```

```

US-09-974-974-17
; Sequence 17, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; FILE REFERENCE: target RNA by recognizing another molecule
; CURRENT APPLICATION NUMBER: US/09/974,974
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 138
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal T-MZL
US-09-974-974-17

Query Match          57.4%; Score 81; DB 11; Length 138;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGUGAGUGUUAUACACGUGCCUACACGCGAAAGGUCGCCGG 60
Db 1 ACCGUGUUCGUGAGUGUUAUACACGUGCCUACACGCGAAAGGUCGCCGG 60
QY 61 UUCGAAACCGGCGACUACAAA 81
Db 61 UUCGAAACCGGCGACUACAAA 81

RESULT 3
US-10-027-632-13958/c
; Sequence 13958, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13958
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13958

Query Match          46.7%; Score 65.8; DB 13; Length 704;
Best Local Similarity 71.8%; Pred. No. 1.2e-13;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

US-10-027-632-13959/c
; Sequence 13959, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13959
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13959

Query Match          46.7%; Score 65.8; DB 13; Length 704;
Best Local Similarity 71.8%; Pred. No. 1.2e-13;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

US-10-027-632-13960/c
; Sequence 13960, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13958
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13958

Query Match          46.7%; Score 65.8; DB 13; Length 704;
Best Local Similarity 71.8%; Pred. No. 1.2e-13;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 3 CGUUGGUUCCGUAGUGUUAUACACGUGCCUACACGCGAAAGGUCGCCGGU 62
Db 301 YGCAGGTTCCGTAGTGTATACGCTGCGCTCACACGCGAAAGGTCGCCGGT 242
QY 63 CGAAACCGGGC 73
Db 241 CGAAACCGGGC 231

RESULT 4
US-10-027-632-13959/c
; Sequence 13959, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13959
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13959

Query Match          46.7%; Score 65.8; DB 13; Length 704;
Best Local Similarity 71.8%; Pred. No. 1.2e-13;
Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGUUGGUUCCGUAGUGUUAUACACGUGCCUACACGCGAAAGGUCGCCGGU 62
Db 301 YGCAGGTTCCGTAGTGTATACGCTGCGCTCACACGCGAAAGGTCGCCGGT 242
QY 63 CGAAACCGGGC 73
Db 241 CGAAACCGGGC 231

RESULT 5
US-10-027-632-13960/c
; Sequence 13960, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13958
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13960

```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 08:02:46 ; Search time 152.75 Seconds  
(without alignments)  
2241.006 Million cell updates/sec

Title: US-09-763-590-2

Perfect score: 141

Sequence: 1 accgugguuuccguagugu.....ggcagcugcgaacgguuuu 141

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	57.4	88	11	US-09-974-974-5
2	81	57.4	138	11	US-09-974-974-17
3	65.8	46.7	704	13	US-10-027-632-13958
4	65.8	46.7	704	13	US-10-027-632-13959
5	65.8	46.7	704	13	US-10-027-632-13960
6	65.8	46.7	704	13	US-10-027-632-13961
7	61.2	43.4	818	13	US-10-027-632-150959
8	61.2	43.4	818	13	US-10-027-632-150960
9	50.6	35.9	603	13	US-10-027-632-135532
10	50	35.5	817	13	US-10-027-632-135520
11	48.4	34.3	871	13	US-10-027-632-148440
12	41.6	29.5	118067	15	US-10-081-327-32
13	40	28.4	11103	12	US-10-056-405-23
14	40	28.4	11103	14	US-10-094-240-23
15	39.6	28.1	322	13	US-10-027-632-272410
16	38.6	27.4	2126	12	US-10-325-107-59

17	37.4	26.5	999	9	US-09-842-552-100	Sequence 100, App
18	37.4	26.5	2336	9	US-09-842-552-102	Sequence 102, App
19	37.4	26.5	5048	11	US-09-884-465A-2	Sequence 2, Appli
20	36.2	25.7	9425	8	US-08-781-986A-87	Sequence 87, Appl
21	36	25.5	440	9	US-09-864-761-10165	Sequence 10165, A
c 22	36	25.5	740	10	US-09-070-927A-846	Sequence 846, App
c 23	35.4	25.1	400	8	US-08-781-986A-3707	Sequence 3707, Ap
c 24	34.8	24.7	400	8	US-08-781-986A-3777	Sequence 3777, Ap
c 25	34.6	24.5	400	8	US-08-781-986A-3809	Sequence 3809, Ap
c 26	34.6	24.5	6591	8	US-08-781-986A-3114	Sequence 3114, Ap
c 27	34.2	24.3	214	9	US-09-815-242-3628	Sequence 3628, Ap
c 28	34.2	24.3	400	8	US-08-781-986A-3650	Sequence 3650, Ap
c 29	34.2	24.3	400	8	US-08-781-986A-3736	Sequence 3736, Ap
c 30	34.2	24.3	449	8	US-08-781-986A-3687	Sequence 3687, Ap
c 31	34.2	24.3	619	8	US-08-781-986A-3571	Sequence 3571, Ap
c 32	34	24.1	687	8	US-08-781-986A-608	Sequence 608, App
c 33	33	23.4	3309400	10	US-09-738-626-1	Sequence 1, Appli
c 34	31.2	22.1	508	10	US-09-917-800A-319	Sequence 319, App
c 35	30	21.3	4792	10	US-09-863-040-5	Sequence 5, Appli
c 36	29.6	21.0	1218	10	US-09-974-300-308	Sequence 308, App
c 37	29.4	20.9	780	10	US-09-738-626-750	Sequence 750, App
c 38	29.2	20.7	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 39	29	20.6	6526	12	US-10-311-455-2210	Sequence 2210, Ap
c 40	28.8	20.4	5109	11	US-09-962-298-2	Sequence 2, Appli
c 41	28.6	20.3	124884	11	US-09-913-514-1	Sequence 1, Appli
c 42	28.6	20.3	124884	12	US-10-288-823-76	Sequence 76, Appli
c 43	28.6	20.3	125157	11	US-09-913-514-2	Sequence 2, Appli
c 44	28.4	20.1	611	13	US-10-027-632-199163	Sequence 199163,
c 45	28.4	20.1	611	13	US-10-027-632-199164	Sequence 199164,

#### ALIGNMENTS

#### RESULT 1

US-09-974-974-5  
; Sequence 5, Application US/09974974  
; Publication No. US20030013095A1  
; GENERAL INFORMATION:  
; APPLICANT: Kazunari TAIRA  
; APPLICANT: Masashi WARASHINA  
; APPLICANT: TOMOKO WARASHINA  
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/974,974  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: JP 2000-313320  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 88  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: tRNAval promoter sequence  
US-09-974-974-5

Query Match 57.4%; Score 81; DB 11; Length 88;  
Best Local Similarity 100.0%; Pred. NO. 2.7e-19;  
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCUGUGUUCGGUAGUGUGUACGUCGUCGACGCGAAGGCCGCGG 60

Db 1 ACCUGUGUUCGGUAGUGUGUACGUCGUCGACGCGAAGGCCGCGG 60

Qy 61 UUCGAAACCGGCGACUACAAA 81

Db 61 UUCGAAACCGGCGACUACAAA 81

#### RESULT 2